Exploring an enigma: the geographic and temporal origins of the Western Ghats flora

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Failure is not the end, it is a necessary part of the path.

Eno Cordova

Declaration

I declare that this thesis has been composed solely by myself and that it is has not been submitted, in whole or in part, in any previous application for a degree. Except where states otherwise by reference or acknowledgment, the work presented is entirely my own.

Madhavi Sreenath

31 May 2023

Abstract

The Western Ghats are an ancient mountain range with an origin dating back to the Late Jurassic, with an extraordinarily diverse and endemic flora. The biodiversity of these sky islands has been influenced by the separation of India from Gondwana during the Late Jurassic period, and its ultimate collision with the Eurasian plate in the late Cretaceous. As a consequence, the flora of the Western Ghats has the potential to have accreted from several regions, including Africa, the Himalayas, Continental Asia, and the Sunda Shelf. There is an emerging paradigm of tropical floras being geologically young and being driven by high rates of species turnover. However, the unique journey of the Indian subcontinent alludes to the presence of an entirely unique floristic diversity in the Western Ghats, which has not been empirically studied in depth to date. The aim of this thesis is to understand the temporal and geographic origins of the Western Ghats flora. A herbarium genomics approach was employed (Whole Genome Sequencing) to assemble DNA regions of species native or endemic to the Ghats and incorporate them into existing phylogenetic datasets of plant families with wider tropical distributions. Time-calibrated phylogenies and ancestral range evolution models were used to provide a synthetic view of the flora's origins using the families *Annonaceae*, *Begoniaceae*, *Chloranthaceae*, *Dipterocarpaceae*, *Ebenaceae*, *Lauraceae*, *Sapotaceae*, and *Zingiberaceae* as representatives. The ancestral area reconstructions show that the Western Ghats flora originated predominantly from the regions of Continental Asia and the Sunda Shelf during the Miocene-Pliocene period, showing a flora strongly influenced by geologically recent dispersal rather than ancient vicariance.

Lay Summary

In a world where biodiversity loss has become an endless challenge, learning all that we can about our forests is important. The focus of this study was to explore the geological ages and geographic origins of the unusual plants in the mystical Western Ghats of India. The Ghats are a tropical mountain range, situated between the western coast of India and the Deccan Plateau. They were formed when the landmass of India separated from the supercontinent Gondwana in the Late Jurassic about 150 million years ago. They are over 1,600km long, with the highest peak standing over 2,500 m above sea level. These tropical rainforests are home to a vast diversity of flora and fauna and account for one of thirty-six biodiversity hotspots in the world. There are approximately 1,200 species of plant found nowhere else in the world present in the Western Ghats today.

Recent studies on geologically younger tropical montane systems such as those of the Andes and the Malesian Archipelago show plant diversity in these ranges is geologically young with high rates of species turnover. The Western Ghats unlike these ranges are geologically older and carry with them the potential for a very different story. When the Indian subcontinent separated from Gondwana, it embarked on a c.100 Ma voyage across the Tethys Sea, encountering cycles of extreme climate, volcanism, a meteor collision, and mass extinctions along the way. Instead of having a young flora, there is the possible retention of plants from the ancient continent of Gondwana. Coupled with the chaotic history of the subcontinent, this gives the potential for the presence of an entirely unique floristic diversity in the Western Ghats.

This study looks to explore the ages and origins of the unique plants of the Ghats with the help of time-calibrated evolutionary trees (phylogenies) and ancestral area reconstructions using eight flowering plant families as representatives. DNA was extracted from samples of from endemic or native taxa from the Ghats and used to create dated phylogenies for the plant families *Annonaceae*, *Begoniaceae*, *Chloranthaceae*, *Dipterocarpaceae*, *Ebenaceae*, *Lauraceae*, *Sapotaceae*, and *Zingiberaceae.* The ancestral area reconstructions showed the flora of the Western Ghats to have originated in the Miocene-Pliocene period starting about 23 million years ago, largely from the regions of Continental Asia and the Sunda Shelf by methods of dispersal.

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To old friends and family, and new.

May the force be with you.

Chapter One

Introduction

Setting the Stage

Bhavani Range, Silent Valley National Park, Kerala, August 2022.

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1.1 Introduction

Plant biodiversity is unequally distributed across the globe, with some areas having much higher species richness than others, particularly tropical regions. This high species richness closer to the equator (the latitudinal diversity gradient (LDG)), is likely caused by multiple factors and has been in existence for more than 100 Ma (Willig et. al, 2003). Hypotheses proposed to explain the LDG include those based on environmental factors, such as environmental stability and productivity (Pianka, 2010; Wright, 1983), as well as those based on historical factors, such as speciation rates (Gaston and Blackburn, 1996). Within the LDG, disproportionately high species numbers are a feature of tropical montane regions with diversity peaking at the intermediate elevations (Schwery et al., 2015). Similar mechanisms to those underpinning the LDG have been suggested to account for this pattern, albeit at a smaller scale (Pianka, 2010). In addition to species richness, the floristic composition of tropical floras varies from region to region, with otherwise functionally similar vegetation types being composed of very different species cohorts.

Explaining these deviations from the null hypothesis of everything being everywhere is a key question in the field of biogeography, and to answer it we need to know where the species in these hotspots have come from in terms of their age and geographic origin, as well as the relative influence of vicariance, dispersal and in-situ diversification on the build up of diversity. A phylogenetic approach has shown that for plants, global patterns of distribution are potentially driven more by dispersal than vicariance (Sanmartín and Ronquist, 2004). Mountain ranges such as the Andes, the Himalayas, and the Afromontane and Malay archipelagos are relatively well studied with respect to investigations of their age and origin of flora. A paradigm is emerging of these montane floras as being geologically young and mobile (Atkins et al., 2020; Gizaw et al., 2016; Madriñán et al., 2013). However, these are all geologically young ranges and vicariant and relict floras are not a likely hypothesis for them. To fully understand the remarkable species richness and endemism of tropical montane floras, investigations of geologically older systems are needed, hence the focus of this project is the age and origin of the flora of the magnificent Western Ghats of India.

1.2 The Indian Subcontinent through the ages

1.2.1 Pangea and Gondwanaland, and the birth of the Indian Subcontinent

The biological history of the Western Ghats is tightly entwined with the history of the Indian subcontinent itself. The subcontinent of India contains the Dharwar Craton, an ancient mass of crust and lithosphere which is c.3.2 billion years old and makes up most of Peninsular India (Lal, 2016; Pandey, 2014). Approximately 340 million years ago (mya) the landmasses of Euroamerica and Gondwana along with the Ural Mountains (295 mya), and fragments of China, Tibet, and Southeast Asia combined to form the supercontinent Pangea (Cox et al., 2016). This supercontinent then separated into Laurasia and Gondwana (Klaus et al., 2016; Veevers, 2004) c.200 – 230 mya (Müller et al., 2016). Between these two existed a body of water referred to as the Tethys Sea (Cox and Moore, 2005). The geological landmass of Gondwana then proceeded to disperse into the (sub)continents of South America, Africa, India, Antarctica and Australia in a process that began approximately 160 mya (Prasad *et al.*, 2009).

Post this separation the landmass began its mega-annus voyage across the Tethys Sea towards the Eurasian plate (Briggs, 2003; Mateo et al., 2017). India separated from Madagascar c.96-84 mya due to the Marion hotspot plume, and continued with its upward journey post this split (Briggs, 2003). The Marion hotspot plume is said to have aggravated and induced the split, prior to which Madagascar was sliding south along the faulted edge of India (Briggs, 2003). The subcontinent separated from the Seychelles c.65 mya and collided with the Eurasian plate c.55 mya forming the Himalayas (Briggs, 2003). There is tilt to the Indian subcontinent that occurred first when it split from Madagascar and then later when it collided with Eurasia (Subrahmanya, 1994). As the landmass moved northeast it rotated anti-clockwise, this rotation became more pronounced after it split from the Seychelles (Gnos *et al.*, 1997).

The Late Cretaceous period witnessed global mass extinctions (Keller, 2008; Samant and Mohabey, 2014). The subcontinent of India witnessed an enormous volcanic event that is thought to have magnified these extinctions (Chatterjee and Rudra, 1996; Joshi and Karanth, 2013). It has also been suggested that these mass extinctions were exacerbated by meteor collisions at the time, as the impact of these collisions may have made the effects of eruption more pronounced (Chatterjee and Rudra, 1996; Morley, 2000). The Deccan traps cover most of northern peninsular India and parts of central India extending out into the Arabian Sea (Bhatia et al., 2021; Chatterjee and Rudra, 1996). They sit just above the Dharwar Craton and are one of the largest basalt flood plains (Joshi and Karanth, 2013). The lava from this eruption covered much of northern peninsular India implying south India became a biological refugia, retaining wet forest taxa of the area (Joshi and Karanth, 2013). Evidence of this wet forest taxa has been found in perfectly preserved fossils in the Deccan Traps (Bhatia et al., 2021; Morley, 2000; Rust et al., 2010).

Now, the country sits between the Indo-Malayan, Afro-tropical and Eurasian biogeographic regions (Reddy et al., 2015). Logic dictates that upon separation the Indian landmass was subjected to a period of isolation where floral or faunal exchange would have been incredibly rare, however there is fossil evidence to show otherwise (Bossuyt, 2004; Briggs, 2003; Morley, 2018).

1.2.2 Formation and geography of the Western Ghats

India separated from the supercontinent Gondwana between the Late Jurassic and early Cretaceous period (Briggs, 2003; Chatterjee et al., 2013) resulting in the formation an extremely large and distinct mountain range – the Western Ghats (Figure 1.1). Its subsequent collision with the Eurasian plate created another equally distinct and large range – the Himalayas (Ali and Aitchison, 2008; Chatterjee et al., 2013). The Ghats being the older of the two are really an escarpment of the Deccan plateau, they are the result of shearing, of the Indian landmass from the rest of Gondwana (Gunnell, 1997; Radhakrishna et al., 2019; Ray et al., 2009). This faulted edge range is one of the oldest tropical mountain ranges in the world (c.150 mya) and when combined with the island of Sri Lanka is considered one large biodiversity hotspot (Bossuyt, 2004). They span a total length of 1,600 km running from the state of Gujarat in the north to the states of Kerala and Tamil Nadu in the south (Gunawardene *et al.*, 2007). This discontinuous mountain range is bordered by the Western coast and the Arabian Sea on the left and the Deccan Plateau on the right. The entire mountain chain can be divided into three major sections – the Northern, Central and Southern Western Ghats (Joshi and Karanth, 2013).

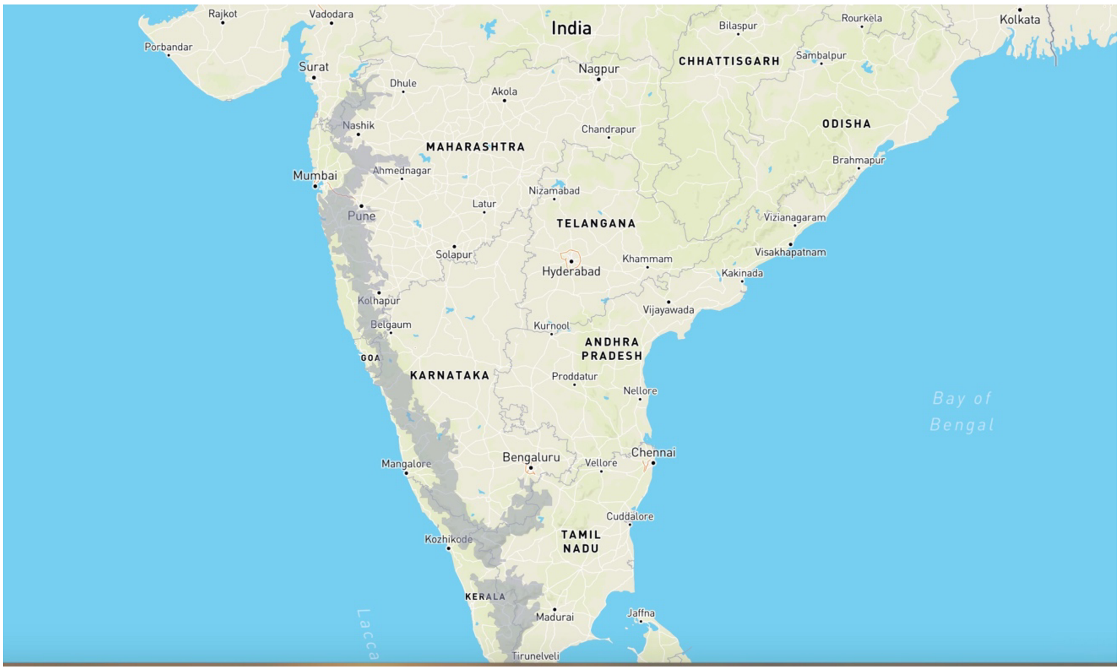

Figure 1.1: Peninsular India with the colour grey demarcating the boundaries of the Western Ghats.

Image taken from indiabiodiversity.org.

The range sometimes called sky islands (Robin *et al*., 2010) house four known and named gaps – the Goa, Moyar (Mysore), Palakkad (Palghat) and Shencottah gaps (Figure 1.2). Each break has a different geological age and size (Robin *et al*., 2010). The subcontinent has three shield separated by three gorges – (1)Moyar-Bhavani Shield; (2) Palghat-Cauvery Shield, and (3) Achankovil Shield; all of which cut into the Ghats (Lal, 2016; Sacks et al., 1997). The Goa gap was formed in the late Cretaceous period (Robin *et al*., 2010) and shares a boundary with the southern edge of the Deccan Traps (Van Bocxlaer et al., 2012). The Moyar Gorge or Mysore Ditch is a valley with an average depth of c.450m and is the river basin for the Moyar river a tributary of the Kaveri (Anoop et al., 2010). The widely known Palghat or Palakkad gap is a 30-40 km wide gorge in the Southern Western Ghats (Robin *et al*., 2010; Joshi and Karanth, 2013). The 7km wide Shencottah gap is located further south of the Palghat gap (Robin *et al*., 2010). The severely fragmented nature of this range gives potential for biodiversity to vary throughout it. Studies have found biodiversity variation within and on either side of these gorges (Anoop *et al*., 2010; Robin *et al*., 2010; Rajasri *et al*., 2017).

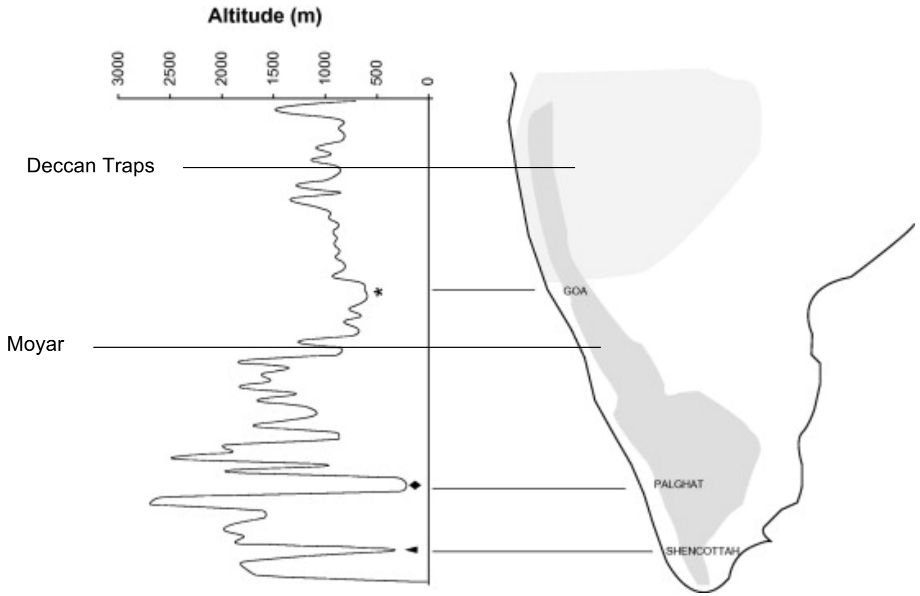

Figure 1.2: Peninsular India showing the Western Ghats in dark grey.

The Deccan Traps in light grey and lines extending outwards to show breaks in the chain. Image taken from (Van Bocxlaer et al., 2012) and edited to show the Moyar or Mysore Gorge whose approximate location was taken from (Meißner et al., 2002).

1.2.3 Topography and Climate

India is more commonly thought of as a tropical country. In reality only the peninsular portion of the country lies in the tropical belt while its upper quarter lies in the temperate belt (Morley, 2000). In terms of the climate this translates as the subcontinent being a gradient of per humid to seasonal depending on latitude. High biodiversity within the country can be attributed to the heterogenous nature of environments across its latitude (which affects climate and temperature) and terrain. India has a wide range of physical features ranging from mountains to deserts. Relief features in the country are the Northern Plains, the Coastal Plains, the Thar Desert, the Deccan Plateau, the Western Ghats, Eastern Ghats, part of the Himalayas, the Gir, Aravalli, Satpura and Vindhyan mountain ranges (Mani, 1974). The Western Ghats also known as the Nilgiri, Cardamom or Sahyadri hills have a total of 74 peaks. The tallest peak Anaimudi is located in the state of Kerala standing at an elevation of 2,695 m above sea level (Rajesh and Prakashkumar, 2012) while the second tallest peak, Doddabetta, Tamil Nadu (Suprit and Shankar, 2008) stands at an elevation of approximately 2,637 m above sea level (Rajesh and Prakashkumar, 2012).

The subcontinent witnesses an extended monsoon from June to December. The monsoons are responsible for water availability within the country, keeping most of the rivers and their surrounding lands from drought. The Western Ghats are the first barrier rain bearing clouds from the Arabian Sea encounter on the peninsula (Gunnell and Fleitout, 1998; Venkatesh and Jose, 2007), making them an excellent sanctuary for megathermal wet forests. Together with the Himalayas, the Ghats responsible for orographic rain over the country (Gunnell and Fleitout, 1998; Morley, 2003). Rainfall abundance has been found to vary throughout these ranges as well (Venkatesh and Jose, 2007). The combination of the subcontinents topographic diversity, climate and water availability makes for a very diverse flora and fauna in its last remaining rain forests, i.e., the Western Ghats and the Himalayas.

1.3 A Rich and Endemic Biota

1.3.1 Floristic Biodiversity

Figure 1.3: Madapura Range, Kodagu District, Karnataka, September 2022.

The combination of its age, latitude, topography and climate makes the biodiversity of the Western Ghats (Figure 1.3) unique (Dray, 2003; Sundarapandian and Swamy, 2015). It is home to approximately 5,588 species of plants of which there are c.1,200 that are endemic (Prakash, 2015). Endemism is higher in the south past the Palghat gap (Davidar et al., 2005; Gopal et al., 2023; Ramesh et al., 2010). Studies conducted in the Ghats have indicated that the floristic diversity of the region is correlated with seasonality (Dray, 2003; Gunawardene *et al.*, 2007; Ramesh *et al.*, 2010)The season between the two monsoon events is said to play a major role in the floristic composition of the subcontinent (Davidar *et al.*, 2005). Vegetation in the Ghats varies depending on the area and the amount of rainfall it receives. The Western Ghats is a combination of montane, evergreen, scrub and deciduous forests, and grasslands (Anoop et al., 2010; Reddy et al., 2015; Sundarapandian and Swamy, 2015).

Each gap in the mountain chain plays a significant role in the climate and accordingly their vegetation (Anoop *et al.*, 2010; Rajasri *et al.*, 2017). Biodiversity is different on either side as well as within these gorges (Anoop *et al.*, 2010; Robin *et al.*, 2010; Rajasri *et al.*, 2017). The flora in the Southern Western Ghats is said to be similar to the flora of Sri Lanka (Gunawardene et al., 2007). Similarities in the flora are seen in the lowland dry forests of Sri Lanka and the Western Ghats (Gunawardene et al., 2007). The Ghats are an area of high and unequally distributed biodiversity (Prasad *et al.*, 2009). This unequal distribution and clustering of biodiversity forms hotspots scattered throughout the Ghats adding to its already non-homogenous flora.

1.3.2 Faunal Biodiversity

High rates of endemism of night frogs (*Nyctibatrachidae*) developed within the Ghats due to their prolonged period of isolation in the Cretaceous, along with minimal interactions with other landmasses (Van Bocxlaer et al., 2012). A similar trend of endemism having evolved in isolation was observed in a clade of pig-nosed frogs (*Nasikabatrachidae*) from the Jurassic period which have descendants in the Southern Western Ghats (Dutta et al., 2004). That India retained components of biodiversity from Gondwana is also evidenced from studies of another primitive amphibian, *Philautus*, in the Central Western Ghats (Gururaja et al., 2007) and the centipede genus *Ethmostigmus* (Joshi and Edgecombe, 2019).

1.3.3 A Biogeographic Conundrum

Tropical rainforests have the potential to be both refugia and areas of recent diversification, making them a combination of both vicariant and dispersed floras. A phylogenetic approach has shown that for plants biogeographic patterns are driven more by dispersal than vicariance (Sanmartín and Ronquist, 2004). Having once been contiguous with the East coast of Africa and Madagascar, the Western Ghats have many potential biogeographic links. Their connections to the landmasses of Africa, Antarctica, Australia, Madagascar, and the Seychelles indicate the potential for having retained Gondwanan elements (Morley, 2000) by virtue of vicariance. This is evidenced by the several lineages of Gondwanan fauna recently found in the Ghats (Dutta et al., 2004; Johnson et al., 2022; Joshi and Edgecombe, 2019; Joshi and Karanth, 2013; Van Bocxlaer et al., 2012). However, their somewhat isolated movement through the latitudes over the geological epochs suggest their flora having changed quite dramatically over the last 100 Ma, as unlike fauna, plant distribution ranges are potentially influenced by their better ability to disperse. Until recently studies with respect to age and origin of biodiversity in the Ghats have predominantly focused on fauna, leaving a research gap for historical biogeographic studies on the flora.

Much of the research on tropical montane systems has focused on regions that are geologically young, such as the Andes and the Malesian Archipelago. In comparison, the Western Ghats are much older, and their flora may harbour older elements. Through the geological epochs, the Ghats have witnessed severe climate change, volcanism, global mass extinctions, etc. They have also experienced floral and faunal exchange via dispersal (Morley, 2018) and the evolution of endemics as a result of isolation (Chatterjee et al., 2013), making their flora entirely unique. The fantastical journey of the Indian subcontinent alludes to the presence of an entirely unique floristic diversity in the Western Ghats, that has not been given enough attention until recently.

1.4 Aim and Objectives

1.4.1 Aim

The aim of this thesis is to understand the temporal and geographic origins of the Western Ghats flora. This can be achieved using dated molecular phylogenetic techniques and biogeographic modelling, showing the build-up of species over geological time from areas surrounding the Indian subcontinent.

1.4.2 Objectives

Sampling design**:** Build a primary checklist of the flora of the Western Ghats to identify angiosperm families to use as biogeographic models. Chose families representing a range of growth forms and geological ages and have existing datasets that can be built upon with taxa native or endemic to the Western Ghats. Use taxa from the selected families for the following objectives.

DNA sequencing and assembly**:** Extract DNA from herbarium and field samples from samples of the selected families native or endemic to the study area, and perform genome skimming using next generation short-read sequencing. Assemble DNA regions matching existing datasets for each family and align all samples.

Phylogenetics**:** Produce time calibrated phylogenies for each family using the software package BEAST (Suchard et al. 2018) based on secondary calibrations.

Biogeographic reconstructions**:** For the selected families, reconstruct ancestral areas across their dated phylogeny using the package BioGeoBEARS (Matzke, 2013).

Data synthesis**:** Collate ages and areas of origin for each immigration event into the Western Ghats from this study and other published research to show the overarching patterns of arrival into the region.

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Chapter Two

Methods

Leaves to Trees

Western Ghats, Kodagu District, Karnataka, August 2022.

List of Figures and Tables

2.1 Checklist

The Western Ghats are home to approximately 5,588 species of native plants of which c.1,200 are endemic to the region (Nayar et al., 2014; Prakash, 2015). To better understand the diversity of these sky-islands, a checklist was collated from published studies and previously created databases generated for the area. Where available, each record included the following details – species name, family, location, state, district, altitude, latitude, longitude, endemicity, basis of record, and source of record. The most recent version of this working checklist (Appendix A.2) has approximately 11,878 specimens with roughly 5,000 species for a total of 177 families, with species diversity being highest in the Southern Western Ghats. It elaborates how the Western Ghats are a truly biodiverse tropical mountain range that are a key element to our understanding of tropical rainforests. The checklist was used to evaluate and identify the best taxa to be used as representatives for this study.

2.2 The Chosen Families

The eight chosen families were spread across the Angiosperm Phylogeny Group (APG) IV (The Angiosperm Phylogeny Group, 2016) phylogeny (Figure 2.1) covering a range of habits and ages. Families were chosen based on biogeographic importance – prior existence on the Gondwanan landmass and their potential ability to corroborate a vicariant origin flora in the Western Ghats. Each family was also chosen for this project based on the availability of viable legacy data, in the form of existing sequence data that could be used to make a phylogeny with broad geographic sampling. Table 2.1 provides a list of the families that were chosen, the loci that were used for bioinformatics and the number of taxa this study added to existing phylogenies.

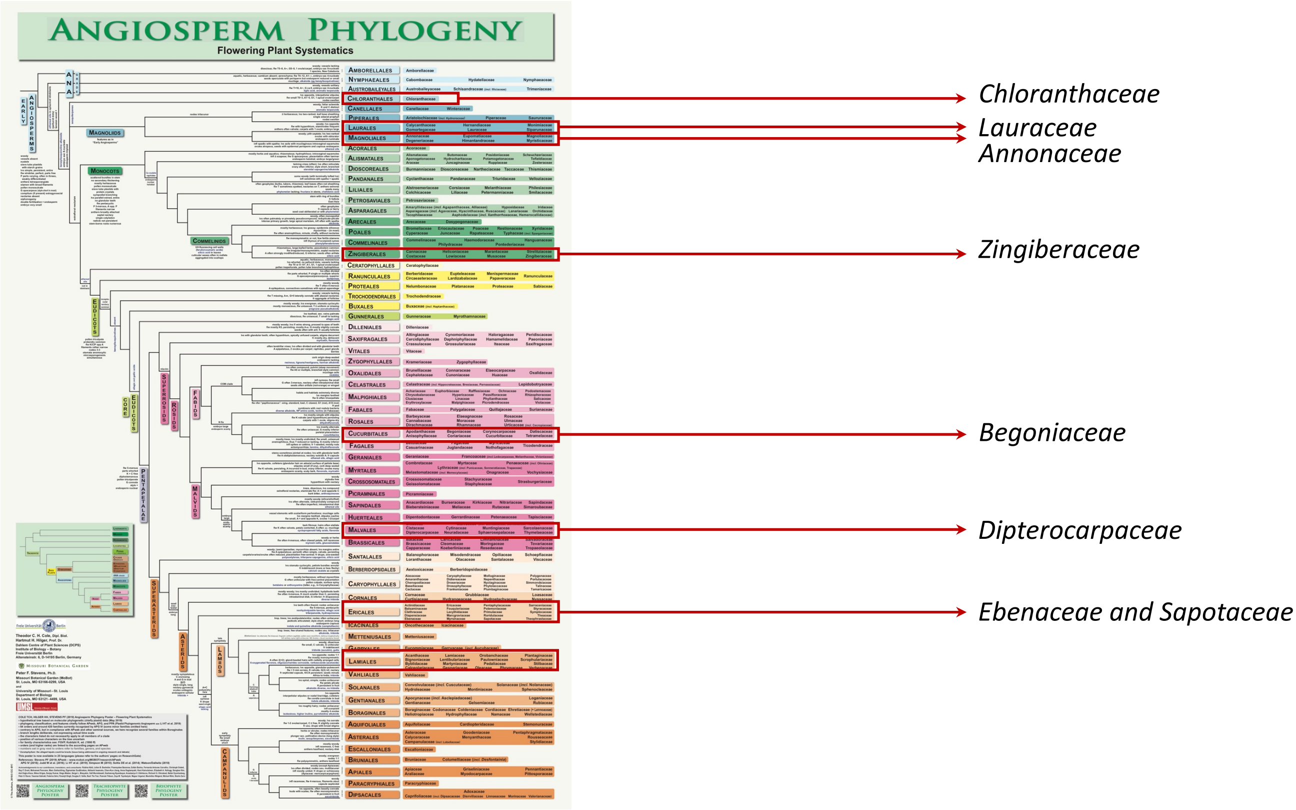


Figure 2.1: Angiosperm Phylogeny (APG IV) indicating the selected families for this project and their placement within the phylogeny.

Annonaceae

Annonaceae is an early diverging pantropical family of the order *Magnoliales* (Stevens, 2001 onwards). The family hosts c.2,400 species and covers a range of habits – lianas, shrubs, and trees (Couvreur et al., 2019; Xue et al., 2020). Taxa are dispersed through birds and primates (Xue et al., 2020). Fossils of *Annonaceae* have been found in the Deccan Traps dating back to the Paleocene epoch (Bhatia et al., 2021; Wheeler et al., 2017), making the family an excellent candidate for the exploration of the Western Ghats flora. There are c.60 species of *Annonaceae* endemic/native to the Ghats (Nayar et al., 2014), 21 of which were examined in this study.

Begoniaceae

Begoniaceae belongs to the order *Cucurbitales* (Stevens, 2001 onwards) and has two genera – the monotypic genus *Hillebrandia* and the pantropical genus *Begonia* L. (Moonlight et al., 2018). The genus *Begonia* L. consists of c.2,120 species (Hughes et al., 2015-) in the form of herbs and shrubs. It is the sixth largest genus in the world

(Moonlight et al., 2018) with much of this species richness found in Asia and America (Dewitte et al., 2011). There are approximately 17 species of *Begonia* L. endemic/native to the Western Ghats (Nayar et al., 2014), 10 of which were included in the final analysis.

Chloranthaceae

Chloranthaceae is an early diverging family that belongs to the order *Chloranthales* (Antonelli and Sanmartín, 2011; Zhang et al., 2015). It has four genera that cover a range of habits – herbs, shrubs, and trees (Doyle and Endress, 2018). The family boasts a rich fossil record from the Cretaceous epoch with c.70 extant species (Antonelli and Sanmartín, 2011; Doyle and Endress, 2018; Zhang et al., 2015). A single taxa is found native to the Ghats (Nayar et al., 2014).

Dipterocarpaceae

Dipterocarpaceae is a pantropical tree family that belongs to the order *Malvales* (Heckenhauer et al., 2017), and dominates the forests of Southeast Asia (Kooyman et al., 2019). It has approximately 695 species with diversity being the highest in Asia (Sanil et al., 2022). Fossil evidence of the family has been found from the Cretaceous – Paleocene epochs (Kooyman et al., 2019; Sanil et al., 2022), along with amber in the Deccan Traps from the Eocene (Rust et al., 2010). The family has both winged and wingless fruit, taxa with winged fruit are wind dispersed (Heckenhauer et al., 2017; Morley, 2018). There are 18 species of *Dipterocarpaceae* endemic/native to the Western Ghats (Nayar et al., 2014; Sanil et al., 2022), 16 of which were examined in this study.

Ebenaceae

Diospyros is the largest genus in the family *Ebenaceae*, order *Ericales*. (Linan et al., 2019; Samuel et al., 2019). It is a pantropical genus that consists of approximately 890 species (Linan et al., 2019), comprising of mostly shrubs and trees (Duangjai et al., 2009). There is fossil evidence of the family from the Cretaceous period (Bansal et al., 2021; Linan et al., 2019). The Western Ghats house approximately 29 species of *Diospyros* (Nayar et al., 2014), of which this study examined 11.

Lauraceae

Lauraceae is an early diverging family that belongs to the order *Laurales* (Stevens, 2001 onwards). The family has c.3.500 species and can be found in the tropical and temperate zones (Chanderbali et al., 2001; Huang et al., 2016; Song et al., 2020). The family boasts a rich fossil history in the Deccan Traps (Bhatia et al., 2021), with potential Gondwanan origins (Chanderbali et al., 2001; Rohwer, 2000). Seeds are dispersed by large fruit eating birds (Stevens, 2001 onwards). There are c.70 or so species endemic/native to the Western Ghats (Nayar et al., 2014), this study examined 17.

Sapotaceae

Sapotaceae is a shrub and tree family that belongs to the order *Ericales* (Anderberg and Swenson, 2003; Stevens, 2001 onwards). The pantropical family has c.1,100 species (Anderberg and Swenson, 2003, 2005). There is fossil evidence for *Sapotaceae* from the Paleocene epoch found in the Deccan Traps (Bhatia et al., 2021). Seeds are dispersed by animals that consume fruit (Stevens, 2001 onwards). 18 species of the family are endemic/native to the Western Ghats (Nayar et al., 2014), this study examined 8.

Zingiberaceae

Zingiberaceae is a pantropical monocot family that belongs to the order *Zingiberales* (Zhao et al., 2022; Stevens, 2001 onwards). This diverse family hosts c.1,200 species (Zhao et al., 2022). There is fossil evidence of *Zingiberaceae* that has been found in the Decan Traps, from the KT boundary, indicating towards a possible Gondwanan origin (Zhao et al., 2022). There are approximately 58 or so taxa of *Zingiberaceae* that are endemic/native to the Ghats (Nayar et al., 2014), 25 of them were examined in this study.

Family	**Loci**	**Number of taxa added**
Annonaceae	matK, ndhF, rbcL, ycf1, atpB, trnS, trnL, and trnH (Xue et al., 2020)	10
Begoniaceae	nadh, ndhF, and trnL (Moonlight et al., 2018)	10
Chloranthaceae	ITS (Zhang et al., 2015)	1
Dipterocarpaceae	matK, trnL, and trnF (Sanil et al., 2022)	1
Ebenaceae	atpB, rbcL, matK, and trnS (Turner et al., 2013)	7
Lauraceae	ITS (Chanderbali et al., 2001; Huang et al., 2016; Song et al., 2020)	17
Sapotaceaeae	ITS (unpublished, Kumarage 2016)	5
Zingiberaceae	matK (unpublished, Kumarage 2016)	15

Table 2.1: Selected families, the respective loci used for bioinformatic and phylogenetic analyses, and the number of Western Ghats taxa that have been added.

2.3 Sample Acquisitions

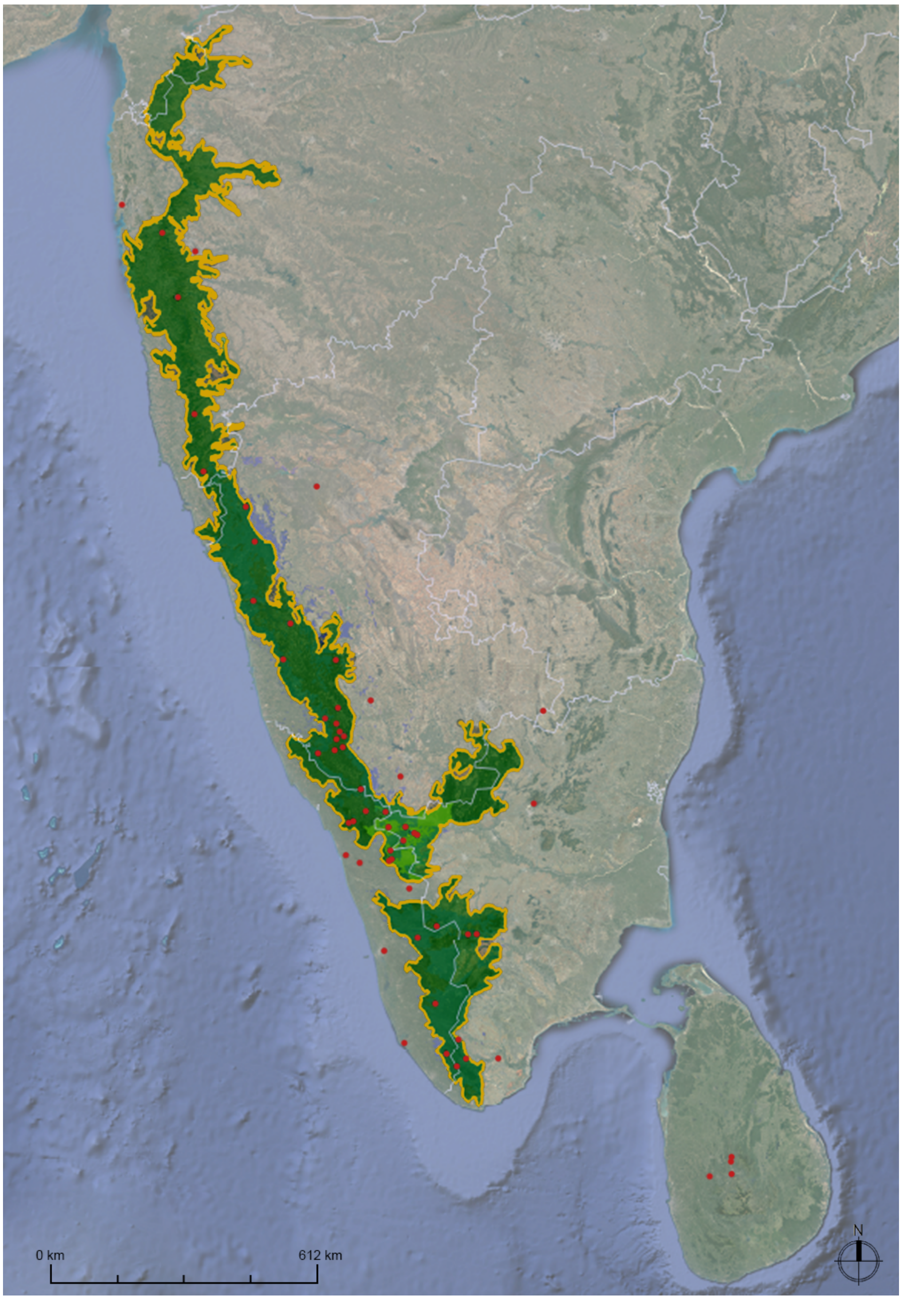


Figure 2.2: Western Ghats boundary map depicting locations of all sequenced samples that were used in this project.

2.3.1 Herbaria

Portions of leaf material were removed from herbarium material using destructive sampling methods. Specimens were acquired from two herbaria – Royal Botanic Garden Edinburgh (RBGE) and Royal Botanic Garden Kew (KEW). Samples were collected from the following angiosperm families – *Annonaceae, Begoniaceae, Chloranthaceae, Ebenaceae, Lauraceae, Sapotaceae and Zingiberaceae.* Samples were chosen based on the quality of the herbarium sheet and the ease of destructive sampling. Ease of destructive sampling being how much damage to the sheet destructive sampling would cause to the integrity of the sheet. Each of these samples were then stored in a grip seal bag and given a sample number, with respective details from the sheet recorded (Appendix A.1). The number of samples for each family varied, largely depending on what was available in the herbaria. The age of these specimens ranged from 50-200 years, a majority of them being colonial collections. The quality of these specimens was also very dependent on the methods of preservation that were used in the field once they were collected. This attributed to contamination that was visible in samples post extraction.

2.3.2 Field

Samples were collected from the Western Ghats forests of Karnataka and Kerala, in territorial forests and protected areas respectively. The total length of the Ghats from Gujarat to Kerala and Tamil Nadu spans c. 1,600 km. Field collections (Appendix A.1) were made over a length of c. 350 km between the states of Karnataka and Kerala. In the state of Karnataka, permission to collect botanical specimens was granted only for territorial forests (forests that do not fall under that category of a wildlife sanctuary or protected area). Collections were made in the territorial forests of the Kodagu district in the talukas of Madikeri and Somwarpet (Figure 2.3). In the state of Kerala, permission to collect botanical specimens was granted for protected areas and wildlife sanctuaries. Collections were made in two major wildlife sanctuaries that differ in forest type, composition, and rainfall – Bhavani Range, Silent Valley National Park (Figure 2.4), and Muthanga Wildlife Sanctuary (Figure 2.5).

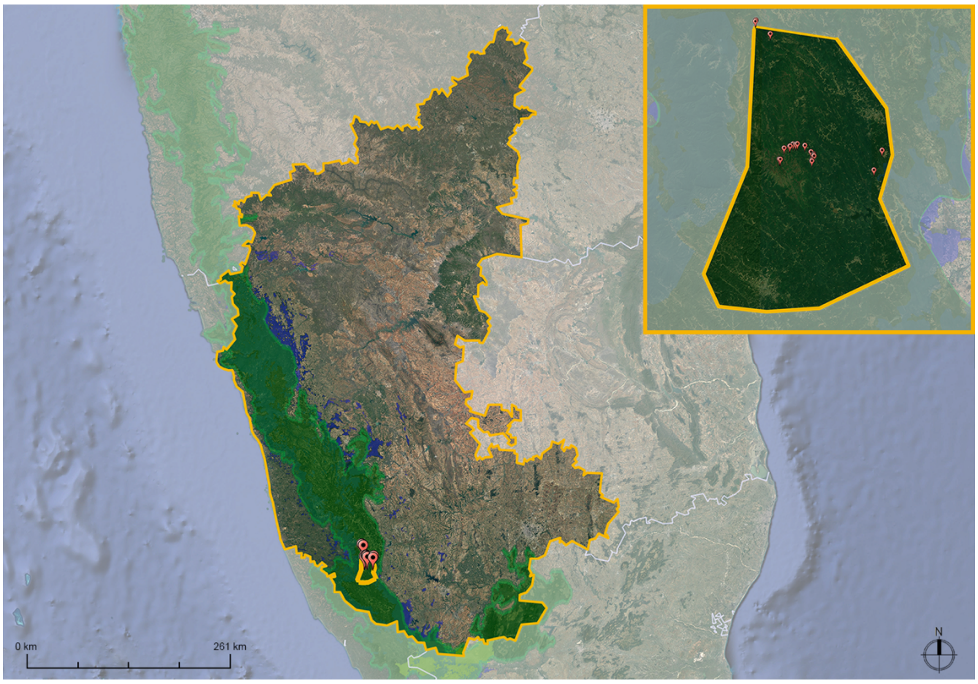


Figure 2.3: Specimen collection locations in the Kodagu district of Karnataka.

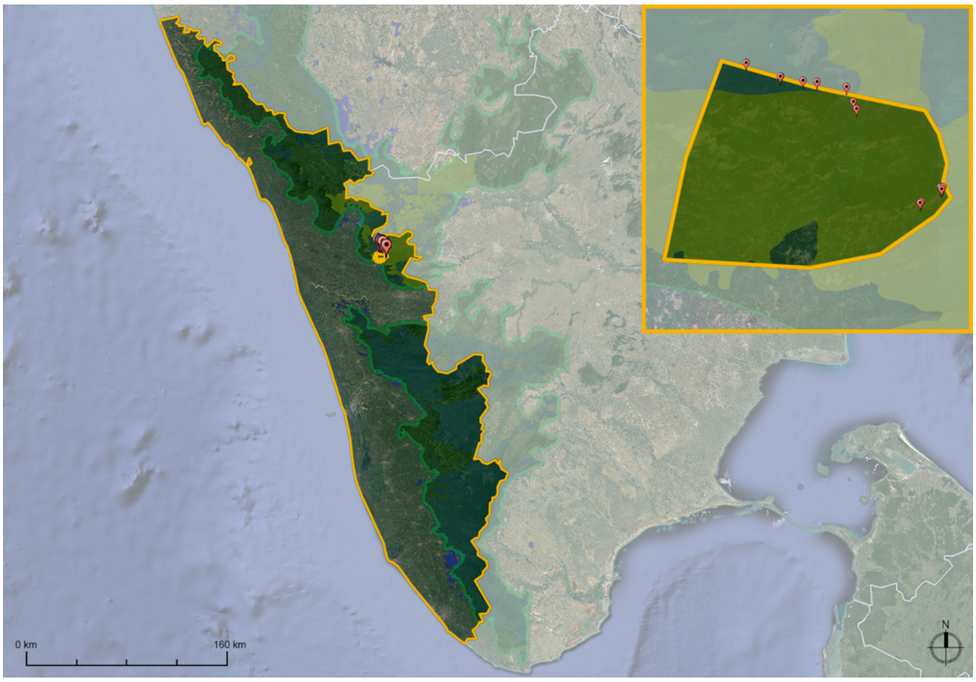


Figure 2.4: Specimen collection locations in Silent Valley National Park, Kerala.

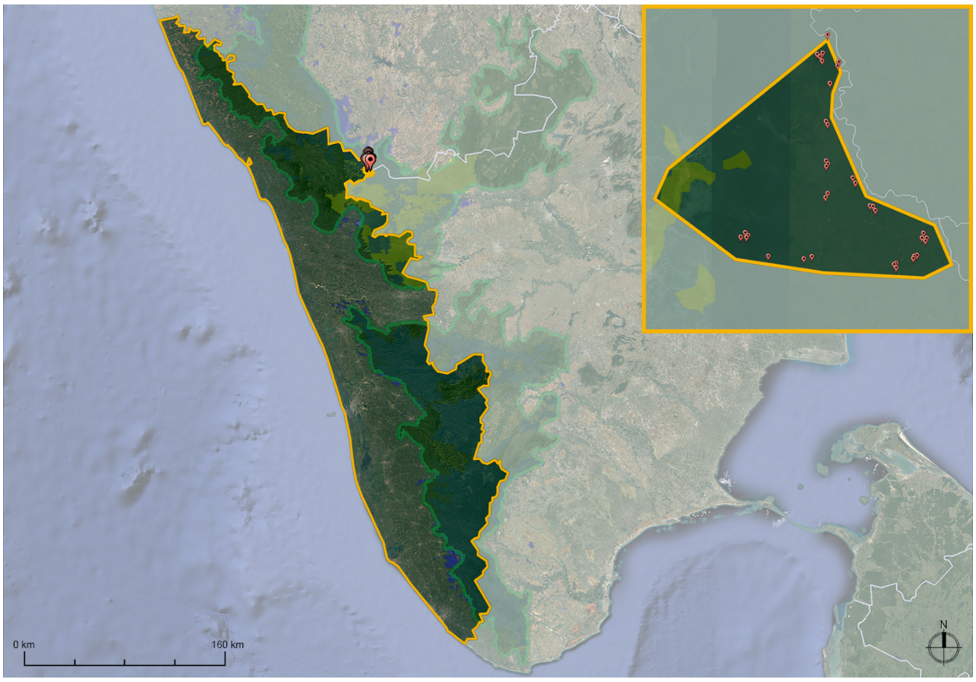


Figure 2.5: Specimen collection locations in the Muthanga Wildlife Sanctuary, Kerala.

Fieldwork was conducted during the monsoon months of August and September 2022. The wetness of the field season greatly affected the preservation of herbarium specimens. Some sheets were lost to mould due to the extremely high moisture content. Samples were collected in two forms – silica dried and herbarium. Where possible herbarium sheets were collected in triplicates for each specimen. Specimens were collected in the field and pressed in newspaper upon moving to a dry location. A leaf sample of c. 5 grams was collected in a tea bag and dehydrated using silica. At each point of collection, an image of the sample, its habit and the GPS coordinates of the area were taken. GPS coordinates were acquired using a Garmin eTex30 set to World Geodetic System 84 (WGS84). Collected specimens will be available at the Botanical Society of India herbarium, as agreed upon with the National Biodiversity Authority of India.

2.3.3 Collaborations

Collaborations with various institutes from around the world has been vital to this project. Sixteen samples of silica dried *Begoniaceae* were received from collaborators at the Calicut University Botanic Gardens (CUBG). An extraction of *Begonia malabarica* was received from the living collections at KEW. Raw sequence data for the genus *Diospyros,* family *Ebenaceae* was exchanged with collaborators at KEW. Multi-fasta alignments and raw sequence data for the family *Annonaceae* were exchanged with collaborators at the Singapore Botanic Gardens (SBG).

2.4 Wet Lab

2.4.1 Extractions

DNA was extracted from 208 herbarium and silica dried leaf material belonging to eight angiosperm families using the Qiagen DNeasy Plant Mini Kit. The manufacturer's base protocol was altered to best fit the sample quality and type.

Herbarium material

DNA from herbarium leaf material was extracted using an altered DNeasy Plant Mini Kit protocol that proved to be highly effective at increasing the yield from highly degraded specimens (Forrest et al., 2019). The manufacturer's protocol was edited for extractions as follows. Samples were stored overnight in mixer mill tubes at -20ºC with two tungsten beads to enable a finer grind. Each sample was extracted as replicates of four. 800µL of Buffer AP1 was added to each tube and the incubation period increased to an hour at 65ºC. 260µL of Buffer P3 was added to each tube and the incubation period altered to 30 minutes at -20ºC. The four replicates were combined and 1.5 times the output volume of Buffer AW1 was added to form a precipitate. The DNA was eluted twice using 0.1 TE solution to acquire a total volume of 65µL of extracted DNA. Some samples of *Begoniaceae* and *Sapotaceae* were subjected to two full rounds of this edited protocol as the DNA yield upon quantification was extremely poor. Sample information for herbarium specimens can be found in the Appendix (Appendix A.1).

Silica dried material

DNA from silica dried leaf collections was extracted using the Qiagen DNeasy Plant Mini Kit. The manufacturer's protocol was edited for the most effective outcome as follows. CUBG samples were stored overnight in mixer mill tubes at -20ºC with two tungsten beads to enable a finer grind. 800µL of Buffer AP1 was added to each tube and the incubation period increased to an hour at 65ºC. 260µL of Buffer P3 was added to each tube and the incubation period was altered to 30 minutes at -20ºC. 1.5 times the output volume of Buffer AW1 was added to form a precipitate. The DNA was eluted twice using 0.1 TE solution to acquire a total volume of 70µL of extracted

DNA. Sample information for CUBG specimens can be found in the Appendix (Appendix A.1)

Field collections

Lab work for field collected samples was conducted at the Conservation Genetics lab at the Ashoka Trust for Research in Environment and Ecology (ATREE), Bengaluru. DNA from silica dried field collections was extracted using the Qiagen DNeasy Plant Mini Kit. The manufacturer's protocol was edited for the most effective outcome as follows. Field collections were freeze dried using liquid nitrogen and powdered using a mortar and pestle. This powder was then transferred to 1.5mL Eppendorf tube. 800µL of Buffer AP1 was added to each tube and the incubation period increased to an hour at 65ºC. 260µL of Buffer P3 was added to each tube and the incubation period was altered to 30 minutes at -20ºC. 1.5 times the output volume of Buffer AW1 was added to form a precipitate. The DNA was eluted twice using 0.1 TE solution to acquire a total volume of 70µL of extracted DNA. Sample information for field collections can be found in the Appendix (Appendix A.1)

Quantification

DNA quality and quantity was assessed using three methods – gel electrophoresis, spectrophotometry (NanoDrop) and fluorometry (Qubit) (Appendix A.1). Samples were quantified post extraction using a DeNovix DS11 FX. Gel images were acquired using an Agilent Tapestation and High Sensitivity D1000 ScreenTape.

2.4.2 Library Preparation

15 samples were chosen for library preparation as a test based on their DNA concentration values. Depending on length of fragments these samples were then sonicated using a Diagenode Bioruptor Pico Sonication Device. Libraries were made using a NEBNext® Ultra™ II DNA Library Prep with beads kit. The libraries were made for half volumes according to the manufacturer's protocol. Library quality and quantity was assessed using a 2100 Bioanalyzer Instrument and a DeNovix DS11 FX. The pooled libraries were sent to the genomics company Novogene for Whole Genome Sequencing for a maximum of 2GB of data per sample. Information on which samples were subjected to in-house library preparation can be found in the Appendix (Appendix A.1).

2.4.3 Whole Genome Sequencing

Whole Genome Sequencing (WGS) or Genome Skimming is the process of using prepared DNA libraries to capture fragments of the genome that can be found without any definition. A total of 147 extraction were sent to Novogene for library preparation and Whole Genome sequencing (Illumina 150BP paired end) for a maximum of 2GB per sample. In the first round 131 herbarium extractions were sent off and 81 samples were returned in the form of viable raw data. 62% percent of the herbarium extractions survived sequencing. In the second round 16 samples were sent off for sequencing and 15 samples were returned in the form of viable data. 50 field collections were extracted and sent to the Bengaluru based company Genotypic for a maximum of 2GB of data per sample. All 50 samples were sequenced and returned in the form of raw data.

2.5 Bioinformatics

Raw Data from multiple sequencing jobs were processed and analysed on the UK CropDiversity – Bioinformatics HPC. In addition to the quality reports provided by sequencing companies, samples were assessed for quality using the package FastQC (Andrews, 2010). All raw data and their intermediate files are currently stored on CropDiversity HPC.

2.5.1 Pipeline

Samples were originally processed using a pipeline that was created using Hyb-Piper (Johnson et al., 2016) as the premise. This pipeline was heavily altered to maximise the output sequence quality as the initial method proved to be highly prone to data loss. The new pipeline was broken into three major parts and are explained in detail below – (i) Plastid region and ribosomal assembly from Whole Genome Sequencing, (ii) *de novo* Assembly using Geneious, and (iii) Concatenation of legacy and new data.

Reference Sequences and Legacy Data

Families were mapped to a reference from a previously published dataset. The reference was a multi-fasta file with several loci for a single species. The loci used to map were entirely dependent on existing datasets and how resolved their subsequent phylogenies were (Table 2.1). This document refers to data from previously conducted studies as Legacy Data. Data from published phylogenies for the families *Chloranthaceae, Dipterocarpaceae, Ebenaceae,* and *Lauraceae* were pulled from GenBank using an R script (Baliga, 2020). The alignment for *Begoniaceae* was taken from Moonlight et al. (2018); the alignments for *Sapotaceae* and *Zingiberaceae* were taken from a currently unpublished PhD thesis (Kumarage, 2016). Further sampling from other published sources was taken from GenBank and added to the *Zingiberaceae* phylogeny. The *Annonaceae* phylogeny was received through collaboration with D.C. Thomas (Singapore Botanic Garden).

Legacy Miner Pipeline

Samples were originally processed using a pipeline (Legacy Miner) that was created with Hyb-Piper (Johnson et al., 2016) as the premise (unpublished, Wilson, 2021). The pipeline is a loop designed to take samples from raw to multi-fasta format using several next generation sequencing (NGS) packages. Samples were run through Trimmomatic 0.39-1(Bolger et al., 2014), Bowtie2 2.4.5 (Langmead and Salzberg, 2012), Samtools 1.9 (Li et al., 2009), and then consensus of the individual gene sequences was called using Kindel (Constantinides and L. Robertson, 2017). The individual genes were then concatenated and aligned using AMAS (Borowiec, 2016) and MAFFT (Katoh et al., 2002) respectively.

Plastid Region Miner for Whole Genome Sequencing

The Plastid Region Miner (PRM) pipeline is a loop that takes whole-genome raw short-read sequence data and outputs it as a Binary Alignment Map (BAM) file containing aligned reads for a chosen DNA region. PRM for WGS goes through the following steps. Samples that had libraries prepared in house were trimmed for adapters using the package Trimmomatic 0.39-1(Bolger et al., 2014) and mapped to a reference using Bowtie2 2.4.5 (Langmead and Salzberg, 2012). Samples that had libraries prepared by a sequencing company were sent directly to Bowtie2 2.4.5 (Langmead and Salzberg, 2012) as they were returned pre-trimmed. Reference taxa were chosen from published alignments, to represent all the regions used in their respective datasets. Chosen reference taxa were close to the extracted species in the libraries. The resulting files were processed and unmapped reads removed to reduce file size using SAMtools 1.9 (Li et al., 2009).

BAM and SAM

Next Generation Sequencing produced large quantities of data and has revolutionised our understanding of our plant phylogenetics (Straub et al., 2012).

The short-read approach used in this study results in millions of reads which need to be assembled to produce desired contigs. Mapped and assembled reads are saved to Sequence Alignment Map (SAM) files or their zipped versions – BAM files (Li et al., 2009). Raw WGS reads mapped and assembled using the Legacy Miner pipeline (unpublished, Wilson 2021) produced extremely patchy contigs, with large portions of viable data missing from the consensus when viewed as their BAM formats. Files when read in their SAM format were far more informative as it was possible to see which bases within reads were either mismatched or marked for clipping.

CIGAR string

SAM files hold the following information – mapped reads, their quality, number of base pairs, etc. in the Compact Idiosyncratic Gapped Alignment Report (CIGAR) string. The CIGAR string is an informative set of numbers and letters, that tells you how many base pairs have matched the references, whether there have been any deletions and whether there have been any insertions. It is usually a number followed by a letter. The numerical value tells you the number of base pairs in the read that have been subjected to a specific function and the letter tells you what has been done to those base pairs. The CIGAR string also indicates how many base pairs in each read have been soft clipped.

Soft Clipping

Soft clipping masks region of reads that do not match the reference gene over a certain threshold (Catchen, 2013), this removes potentially unique variations from the mapped reads which are necessary for phylogenetic analyses. It also tends to indicate that the aligners are largely trying to match the repetitive regions and in doing so possibly misaligning reads. By deleting the variations soft clipping increases the match score for the remaining data which is more congruent to the reference (Catchen, 2013), thereby removing what could be useful data on species variability. To fix and include the soft-clipped data in the consensus, a method of altering the CIGAR strings was devised. BAM files containing mapped reads were subjected to a novel python script (unpublished, Pezzini, 2023; Van Rossum and L. Drake, 2009) that edit the CIGAR string annotations for each read from soft clip (S) to match/mismatch (M). The resulting outputs are unaligned mapped reads in BAM format.

To identify how Geneious dealt with previously soft clipped regions, a BAM file was converted to its SAM format and then viewed on command line. Geneious was found to alter soft clip annotations to insertions (I), so the Python script was edited to reflect this. Conversion of the annotations ‘S’ to ‘I’ did not solve the problem, the resulting consensus files indicated that while the reads were now not trimmed due to soft-clipping, they were misaligned to each other. Although the issue of soft clipping was solved the next step was to ensure the correct alignment of mapped reads using *de novo* assembly.

De novo assembly with command line

de novo Assembly was attempted with the command line assembler Velvet 1.2.10 (Zerbino and Birney, 2008). The use of Velvet for *de novo* assembly proved to be unsuitable due to the number of samples and the number of genes for each sample, as Velvet required the identification of an appropriate kmer value for each gene of each species. To improve efficiency, *de novo* assembly was executed in Geneious with the help of a batch workflow for assembly and consensus calling. Consensus sequences for the individual genes were then stitched together and combined with their respective legacy datasets on the command line.

De novo assembly with Geneious

Unaligned mapped reads were downloaded from CropDiversity HPC and imported without reference files into the bioinformatic platform Geneious 11.1.5. The individual gene files were *de novo* assembled using Geneious’ inbuilt assembler. For each gene the contig with the highest or second highest number of reads was chosen and consensus called with the sequence threshold quality set to 65%. The consensus sequences were exported in fasta format and transferred onto CropDiversity HPC.

Concatenation

Newly assembled and downloaded legacy gene files were first concatenated per species and then a single alignment was generated for the family using the package AMAS (Borowiec, 2016). The resulting multi-fasta file was then aligned with MAFFT (Katoh et al., 2002) and fine-tuned in BioEdit (Hall, 1999).

2.6 Phylogenetics

The following text summarises the principal phylogenetic approach used for the selected families. Maximum Likelihood trees were run for all families on CropDiversity HPC using the package IQ-Tree (Nguyen et al., 2015) with the number of replicates for bootstrap set to 1000 and automatic model selection. Bayesian analysis was run for eight families using the command line version of BEAST v1.10.4 (Suchard et al., 2018). Parameters for Bayesian analyses were taken from previously published studies unless otherwise specified. Files for analyses were generated using BEAST's graphic user interface (GUI) version of BEAUti v1.10.4 (Suchard et al., 2018). The log parameter files were visualised in the GUI version of Tracer v1.7.1 (Suchard et al., 2018) and the command line version of TreeAnnotator v1.10.4 (Suchard et al., 2018) was used to remove burn-in and pick the maximum clade credibility (MCC) tree where possible. Trees were then viewed in FigTree v1.4.4 (Rambaut, 2007-). Node ages were secondary calibrations taken from previously published studies. The following paragraphs provide details of the exact parameters used for the individual families.

Annonaceae

A dated phylogeny of *Annonaceae* was generated with 630 taxa with newly established parameters. The phylogeny had a *Magnoliineae* stem node group that was constrained as monophyletic and an *Annonaceae* crown node group constrained as monophyletic. The substitution model for the tree was set to GTR with the site heterogeneity model set to Gamma + Invariant sites. The number of gamma categories was set to 4 with the clock type set as uncorrelated relaxed clock. The relaxed distribution was set to lognormal for a Yule process tree (Gernhard, 2008). Stem node prior distribution was set to lognormal with a mean of 118.8 (Janssens et al., 2020) and a standard deviation of 1. The crown node prior distribution was set to lognormal with a mean of 100.8 (Janssens et al., 2020) and a standard deviation of 1. Length of the Markov Chain Monte Carlo (MCMC) chain was set to 50,000,000 generations to sample every 1000 generations. Four separate rounds with the exact parameters were run and then combined post. Combined logs of the four runs gave estimated sample size values (ESS) above 100. The four runs were then resampled separately using the GUI version of LogCombiner v1.10.4 (Suchard et al., 2018) at a frequency of 20,000. LogCombiner v1.10.4 (Suchard et al., 2018) was then used to combine the resampled files with a 10% burn-in.

Begoniaceae

A dated phylogeny of *Begoniaceae* was generated with 372 taxa. Four samples from the *Begonia malabarica/dipetala* sample set (Table A.1) have been used in the final *Begoniaceae* phylogeny as taxonomic place holders for the following species – (i) *Begonia malabarica*, (ii) *Begonia dipetala*, (iii) *Begonia fallax*, and (iv) *Begonia hydrophila*. The phylogeny had monophyletic *Hillebrandia* as stem node and a monophyletic

Begonia crown group. The substitution model was set to GTR with the site heterogeneity model set to Gamma + invariant sites and the number of gamma categories set to 4. The clock type was set to uncorrelated relaxed clock with a relaxed distribution for a Yule process tree (Gernhard, 2008). A lognormal prior distribution was set for the crown node with a mean of 24 (Thomas et al., 2012) and a standard deviation of 1. The length of the MCMC chain was set to 50,000,000 generations sampling every 1000 generations. The log file indicated that ESS values were greater than 150. A 25% burn-in was removed before an MCC tree was chosen.

Chloranthaceae

A dated phylogeny was generated using ITS sequences for 44 taxa of the family *Chloranthaceae.* The genus *Hedyosmum* was constrained as monophyletic and established as the stem node group, two crown node groups were constrained for the genera *Chloranthus* and *Sarcandra* respectively. The substitution model was set to GTR with the site heterogeneity model set to Gamma + invariant sites. The number of gamma categories was set to 4 and the clock type to uncorrelated relaxed clock for a Yule process tree (Gernhard, 2008). A lognormal prior distribution was set for the stem node with a mean of 112 (Zhang et al., 2015) and a standard deviation of 1. The length of the MCMC chain was set to 50,000,000 generations sampling every 1000 generations. ESS values were found to be greater than 200. A 25% burn-in was removed before a MCC tree was chosen.

Dipterocarpaceae

A dated phylogeny was generated for the family *Dipterocarpaceae* for 158 taxa. A *Dipterocarpus* crown group was constrained as monophyletic and a second monophyletic crown node ingroup consisting of all *Dipterocarpaceae* was established. The substitution model was set to GTR with the site heterogeneity model set to Gamma + invariant sites. The number of gamma categories was set to 4, with clock type set as uncorrelated relaxed clock for a Birth-Death process tree (Gernhard, 2008). The ingroup prior distribution was set to lognormal with a mean value of 87.5 (Sanil et al., 2022) and a standard deviation of 0.015. A lognormal prior distribution was set for the *Dipterocarpus* crown group with a mean of 52 (Sanil et al., 2022) and a standard deviation of 0.015. Length of MCMC chain was set to 1,000,000,000 generations to sample every 10,000 generations. ESS values were all well above 200. A 10% burn-in was removed prior to a MCC tree being chosen.

Ebenaceae

A dated phylogeny was generated for 228 taxa of the family *Ebenaceae* focused on the genus *Diospyros.* The family *Ebenaceae* was constrained as monophyletic and established as the stem node. Two crown node groups were generated and monophyly established for both. The first group comprised of taxa from New Caledonia while the second group consisted of all *Diospyros*. The substitution model was set to HKY with no site heterogeneity model. A strict clock was established for Coalescent – Constant Size tree (Kingman, 1982). The stem node prior distribution was set to lognormal with a mean of 106.53 (Bansal et al., 2021) and a standard deviation of 1. The *Diospyros* crown node prior distribution was also set to lognormal with a mean of 95.8 (Bansal et al., 2021) and a standard deviation of 1. The New Caledonia node was given a mean of 34 (Turner et al., 2013)and a standard deviation of 1. Length of the MCMC chain was set to 50,000,000 generations sampling every 1000 generations. The log file established ESS values to be greater than 150. A 10% burn-in was removed prior to MCC tree being chosen.

Lauraceae

A dated phylogeny was generated for 183 taxa from the family *Lauraceae*. The family *Ebenaceae* was established as the stem node group and monophyly constrained. Monophyly was established for a crown group consisting of Asian *Cinnamomum*. The substitution model was set to GTR with a site heterogeneity model of Gamma + invariant sites. The number of gamma categories was set to 4 with the clock type set to uncorrelated relaxed clock for a Yule process tree (Gernhard, 2008). A lognormal prior distribution was established for the stem node with a mean of 111.7 (Janssens et al., 2020) and a standard deviation of 1. A lognormal prior distribution was set for the crown group with a mean value of 20.43 (Huang et al., 2016) and standard deviation of 1. The length of the MCMC chain was set to 50,000,000 generations sampling for every 1000 generations. All ESS values were found to be greater than 200. A 25% burn-in was removed before choosing a MCC tree.

Sapotaceae

A time calibrated phylogeny was generated for *Sapotaceae* using 168 taxa. An outgroup consisting of the species *Sarcosperma laurinum* was established as the stem. Monophyly was constrained for the crown node group Ingroup that hosted everything but *Sarcosperma laurinum*. A second group containing everything but the species *Sarcosperma laurinum* and *Eberhardtia aurata* was called Ingroup 1 and constrained for monophyly. Four crown groups were created for *Chrysophylloideae*, *Manilkara* (monophyly), *Mimusops*, and *Sideroxylon*. The substitution model was set to GTR with the site heterogeneity model set to Gamma + invariant sites. The number of gamma categories was established at 4 with an uncorrelated relaxed clock for a Yule process tree (Gernhard, 2008). The prior distributions of all nodes were set to lognormal. The crown group *Chrysophylloideae* was given a mean of 78 and standard deviation of 1. The *Manilkara* crown group was given a mean of 28 and a standard deviation of 1. The *Mimusops* crown group was given a mean value of 42.9 and a standard deviation of 1. The Outgroup node was given a mean of 102 and standard deviation was set to 1. The *Sideroxylon* crown group mean was set to 52.9 and standard deviation to 1. Length of the MCMC chain was established at 50,000,000 generations sampling at every 1000. The log files depicted ESS values greater than 200. A 25% burn-in was established prior to choosing a MCC tree. Node ages were taken from a currently unpublished PhD thesis (Kumarage, 2016)

Zingiberaceae

A dated phylogeny was generated for 238 taxa belonging to the family *Zingiberaceae*. Monophyly was constrained for *Siphonichiliae* and set as stem group. Monophyly was constrained for the crown group *Tamijiae*. A crown group consisting of everything but the stem group and the *Tamijiae* crown group was constrained as monophyletic and called Ingroup. Monophyly was also constrained for a second group called Ingroup 1 consisting of everything but the *Siphonichiliae* stem group. Four crown groups were established for *Alpiniae*, *Globbeae*, *Ridelieae*, and *Zingibereae*. The substitution model was set to GTR with the site heterogeneity model set to Gamma + invariant sites. The number of gamma categories was set to 4 with an uncorrelated relaxed clock for a Yule process tree (Gernhard, 2008). A lognormal prior distribution was set for all calibrated nodes. The *Siphonichiliae* stem node was given a mean 71 (unpublished, Kumarage 2016) and a standard deviation of 1. The *Alpiniae* crown node was given a mean 41.12 (Zhao et al., 2022) and a standard deviation of 1; The *Zingibereae* crown node mean was set to 43.9 (Zhao et al., 2022) and standard deviation to 1. Length of the MCMC chain was established to 50,000,000 generations sampling every 1000. Log file indicated the ESS were greater than 200. A 25% burn-in was removed prior to choosing a MCC tree. Stem node age was taken from a currently unpublished PhD thesis (Kumarage, 2016)

2.7 Biogeography

2.7.1 Geography

Distribution for individual species was scored using information from previous biogeographic studies if available (unpublished, Kumarage 2016; Sanil et al., 2022; Song et al., 2020; Turner et al., 2013; Zhang et al., 2015; Zhao et al., 2022) and the online database Plants of the World Online (POWO, 2023). Absence and presence tables were created for the species found in the dated phylogenies of the eight families from the previous section. Absence in a geographic range was scored as '0' and the presence of the species in a geographic range was scored as '1'. A small number of species were extremely widespread, the scoring for these was limited to the maximum number of geographic ranges for the family, in order to keep run time for the models manageable (Nicholas J. Matzke, 2013). These were scored to include as much of the variation of their range as possible.

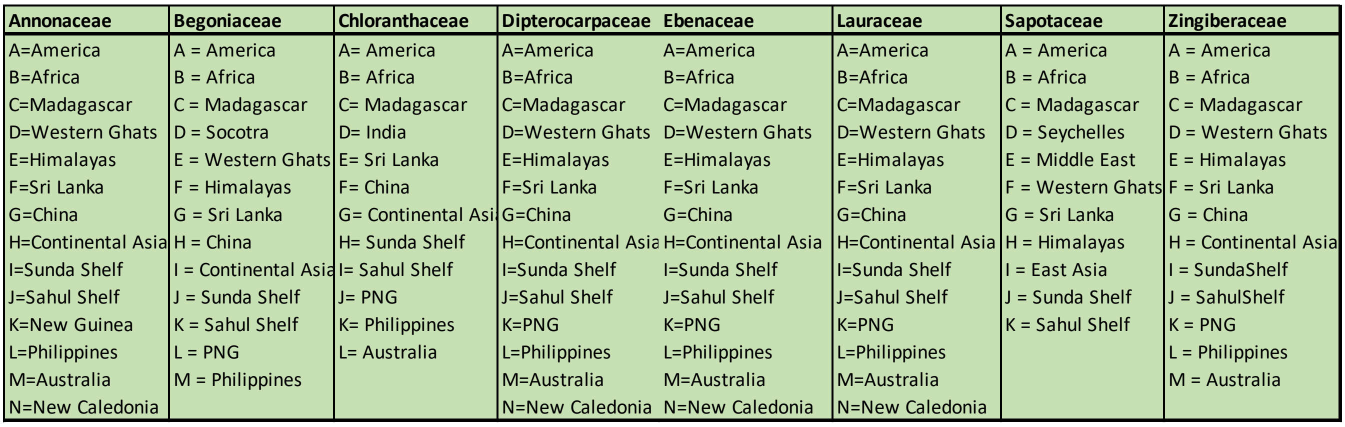
BioGeoBEARS works under the assumption of a fully sampled species phylogeny with one tip per species (Matzke, 2013). However, there were situations of uncertain taxonomy deriving from unresolved species delimitation issues as observed in this study from *Annonaceae*, *Begoniaceae*, *Dipterocarpaceae*, *Ebenaceae* and *Lauraceae.* Each dated phylogeny had a single tip per species unless the tips were identical in name but placed differently in the tree, in which case both samples were kept in the phylogeny. The Western Ghats were scored as a single geographic range as the focus of this study was the Western Ghats, with endemic or native taxa from the region being added to the phylogenies. Geographic areas were designated based on previous classifications and/or the presence of taxa in those areas. The areas were kept as similar as possible across the selected families for the sake of comparability. The following table gives the families, the number of areas and the maximum number of geographic ranges assigned for each family (Table 2.2).

Family	**Total number of areas**	**Maximum number of areas allowed**
Annonaceae	14	3
Begoniaceae	13	2
Chloranthaceae	12	4
Dipterocarpaceae	14	3
Ebenaceae	14	3
Lauraceae	14	3
Sapotaceae	11	3
Zingiberaceae	13	3

Table 2.2: The families, the total number of areas and the maximum number of geographic areas assigned for each family.

2.7.2 BioGeoBEARS

The dated phylogenies from BEAST v1.10.4 (Suchard et al., 2018) and their respective geography tables were used to reconstruct ancestral areas with the R package BioGeoBEARS (Nicholas Joseph. Matzke, 2013). The reconstructions covered six different models – DEC, DEC+J (Nicholas Joseph. Matzke, 2013), DIVALIKE, DIVALIKE+J, BAYAREALIKE, and BAYAREALIKE+J (Matzke, 2014). Founder event speciation or the jump event 'j' model was run as a free parameter. The DEC+J model was used to identify the ancestral areas for the relevant Western Ghats nodes. The following parameters were used for 8 angiosperm families. The ancestral area reconstruction method followed the base protocol with the maximum range size being altered to what fit the geographic scoring of the family the best.



Annonaceae	Begoniaceae	Chloranthaceae	Dipterocarpaceae	Ebenaceae	Lauraceae	Sapotaceae	Zingiberaceae
A=America	A = America	A= America	A=America	A=America	A=America	A = America	A = America
B=Africa	B = Africa	B= Africa	B=Africa	B=Africa	B=Africa	B = Africa	B = Africa
C=Madagascar	C = Madagascar	C= Madagascar	C=Madagascar	C=Madagascar	C=Madagascar	C = Madagascar	C = Madagascar
D=Western Ghats	D = Socotra	D= India	D=Western Ghats	D=Western Ghats	D=Western Ghats	D = Seychelles	D = Western Ghats
E=Himalayas	E = Western Ghats	E= Sri Lanka	E=Himalayas	E=Himalayas	E=Himalayas	E = Middle East	E = Himalayas
F=Sri Lanka	F = Himalayas	F= China	F=Sri Lanka	F=Sri Lanka	F=Sri Lanka	F = Western Ghats	F = Sri Lanka
G=China	G = Sri Lanka	G= Continental Asi	G=China	G=China	G=China	G = Sri Lanka	G = China
H=Continental Asia	H = China	H= Sunda Shelf	H=Continental Asia	H=Continental Asia	H=Continental Asia	H = Himalayas	H = Continental Asia
I=Sunda Shelf	I = Continental Asia	I= Sahul Shelf	I=Sunda Shelf	I=Sunda Shelf	I=Sunda Shelf	I = East Asia	I = SundaShelf
J=Sahul Shelf	J = Sunda Shelf	J= PNG	J=Sahul Shelf	J=Sahul Shelf	J=Sahul Shelf	J = Sunda Shelf	J = SahulShelf
K=New Guinea	K = Sahul Shelf	K= Philippines	K=PNG	K=PNG	K=PNG	K = Sahul Shelf	K = PNG
L=Philippines	L = PNG	L= Australia	L=Philippines	L=Philippines	L=Philippines		L = Philippines
M=Australia	M = Philippines		M=Australia	M=Australia	M=Australia		M = Australia
N=New Caledonia			N=New Caledonia	N=New Caledonia	N=New Caledonia		

Table 2.3: Table indicating the total number of geographic areas scored for each family and the maximum number of areas a species was allowed to be in.

Model Selection

The biogeographic model used across all analysed families for this study was the DEC+J model (Matzke, 2014). For three families the Log Likelihood values indicated that the data favoured the BAYAREALIKE +J over the DEC+J model. However, the BAYAREALIKE +J reconstructions modelled some clades as having multiple ancestral ranges instead of one. This contradicted the range scoring for these families, where many of these taxa were found existing in single ranges. The BayArea model works on the principle of applying the full ancestral range from the previous generation to the next (Nicholas J. Matzke, 2013). One explanation that has been considered for datasets favouring the BAYAREALIKE model over the DEC/DIVALIKE models is that the phylogenies may be missing information in the form of insufficient sampling or species extinction (Nicholas J. Matzke, 2013).

The BAYAREALIKE model is a likelihood based analysis that uses the same free parameters as BAYAREA but excludes three aspects of the original model – dependence on distance, null geographic range, and analysis for several areas (Matzke, 2013). It is not interchangeable with the original BAYAREA model as it works on a likelihood based approach (Dupin et al., 2017; Nicholas Joseph. Matzke, 2013). Of the 8 families a majority of the families favoured the DEC+J models over the DIVALIKE+J or BAYAREALIKE+J models. To be able to compile and compare analyses over several families, a single model is more appropriate and fitted to the reality of current species ranges.

2.8 Leaves to Trees

Eight angiosperm families were chosen for this project based on the availability of viable legacy data in combination with having endemic or native species in the Ghats. These families covered a range of habits and ages. Preserved specimen material was collected from various herbaria, whilst fresh material was acquired from the field. Samples from the herbarium were removed from sheets using destructive sampling methods. Samples from the field were collected in tea bags and placed in silica. All samples were extracted for DNA using the Qiagen DNeasy Plant Mini Kit extraction protocol. These extractions were then sent to a genomics company for library preparation and Whole Genome Sequencing (WGS). The raw sequence data post WGS was mapped to a reference, assembled, and combined with the legacy data to give multi-fasta alignments. These alignments were used to create maximum likelihood and time-calibrated phylogenies. The time calibrated phylogenies were combined with geographic area presence-absence tables for biogeographic model testing.

Figure 2.6 Image depicting the overarching methodology used for all specimen samples in this project.

2.9 Data Synthesis

The overarching aim of this project is to understand the age and origin of the vastly diverse Western Ghats flora, through the summary of phylogenetic data from species and clades endemic or native to the region. Ancestral nodes were established using a conservative approach. Using the BioGeoBEARS phylogenies, and working backwards for each clade, the first node to exclude the Western Ghats was established as the potential ancestral range. Clade ages were then established for these chosen nodes from the dated phylogenies. Clade ages (including 95% HPD range), and ancestral state reconstructions were summarised in a scatter plot and pie chart respectively. Data from eight families which are the focus of this study, plus data from the families *Balsaminaceae*, *Celastraceae*, *Gentianaceae*, *Loranthaceae*, *Orchidaceae*, *Rubiaceae*, and *Piperaceae* (Bajpe et al., 2023; Liu et al., 2018; Neupane et al., 2017; Puri et al., 2016; Sen et al., 2019; Tsai et al., 2020; Yuan et al., 2005) were included.

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Chapter Three

Results

A forest of trees

Mallalli Falls, Kodagu District, Karnataka, August 2022.

List of Figures and Tables

3.1 Data Quality

Quality of extracted DNA varied greatly. Sample quality was tested for, post extraction and post library preparation. The overall DNA quality of herbarium samples was found to be far worse than those of silica dried samples. Herbarium samples were also found to be more prone to contamination. Causes for contamination included method and date of collection, preservation techniques, and storage. Data quality also varied for those samples that survived the process of library preparation and sequencing. The quality and quantity of raw data were generally proportional to each other. Up to 2GB of data were received post sequencing for each sample. Data coverage and quality varied for each sample, and this was visible in two different post-sequencing steps – (i)BLAST post de novo assembly and (ii) sample placement in draft phylogenies. In this dataset quality was seen to be largely dependent on the method of preservation, the age of the specimen and the sample itself. Sample information is provided in the Appendix (Appendix A.1).

3.2 Bioinformatics

3.2.2 Soft Clipping

Samples were mapped to a reference file using Bowtie2 2.4.5 (Langmead and Salzberg, 2012). Upon mapping reads to a reference Bowtie2 soft clips or masks regions of reads that do not match the reference past a defined threshold (Catchen, 2013) deleting potentially useful variation necessary for phylogenetic analyses. When these files are viewed in their Binary Alignment Map (BAM) format they appear as columns of sequence data interspersed with columns of no data, resulting in very large gaps in the final consensus. This was visible across all samples used in this study, no matter the family, species, or sample quality. BAM files were viewed using three different file readers. When viewed using SAMtools tview (Figure 3.1) or Tablet (Figure 3.2) the mapped reads were fragmented.

```
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT       ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGT
ATGAGTGAAATAAAACAGC******TTATAG********AAAAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT       ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT       ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT       ATAAGAGTTAAGCGGAAATAAACATAAT*****AAAAAGATAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAATAGAAC*TTTTATCCC*AAGA   GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGA   ggtt
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT     AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTAT  C*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT       ATAAGAGTTAAGCGGAAATAAACATAAT*****AAAAAGATAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT     AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*G
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATA       AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAA      AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGG        ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT     AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*GGTT
ATGAGTGAAATAAAACAGC******TTATAG********AACAAAGAATTCGCAGTA*******AAAACATTGAGTCTCA*TTTTCTAGGT*******ATAAGAGTTAAGCCGAAATAAACATAAT*****AAAAAGAGAAC*TTTTATCCC*AAGATT*G
```

Figure 3.1: Mapped reads visualised with SAMtools tview.

Figure 3.2: Mapped reads visualised with Tablet 1.21.

Python Script

The presence and absence of data in very distinct columns appeared too clean to be because of trimming based on read quality. In Geneious 11.1.5 columns of viable reads were alternated with columns with pink annotation, which were the soft clipped reads (Figure 3.3). This allowed verification that the soft clipped regions were good quality reads that did not match the reference completely; these regions were annotated pink in Geneious unlike in SAMtools tview or Tablet, where these reads were simply invisible. There existed an option to remove trim annotations in Geneious but this could not be batched. Hence due to the number of genes that needed to be processed there was a need for a more streamlined method involving a command line loop.

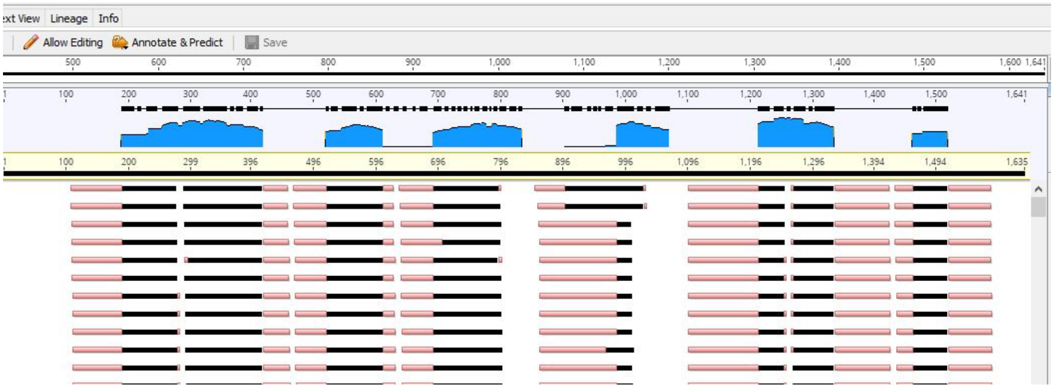


Figure 3.3: Mapped reads from Bowtie2 in BAM format viewed using Geneious 11.1.5.

In the SAM format soft clip annotations were visible in the CIGAR strings of reads. Of 150 bp reads, more base pairs were being clipped than kept. Reads were being clipped sometimes based on single base pair differences. Changing mapping quality and threshold parameters in Bowtie2 and SAMtools proved to be ineffective at resolving this. Therefore, a method of altering the CIGAR strings was devised. This novel method used Python to change read annotations from soft clip (S) to match/mismatch (M) (unpublished, Pezzini, 2023)(Van Rossum and L. Drake, 2009). The resulting outputs were unaligned mapped reads interspersed with aligned mapped reads in BAM format.

This Plastid Region Miner method of mapping and *de novo* assembly proved to be highly effective in improving quality of the assembled sequenced data. It improved the coverage of mapped reads used to assemble each region, and also improved the resolution of samples in their respective phylogenies. Contamination and viability of a consensus sequence for each region was tested using a combination of BLAST and draft phylogenies made with the command line version of IQTREE. Any samples on unusually long branches or in taxonomically suspect locations were removed from the analyses. Appendix Table A.1 indicates samples that were retained/discarded from the final analyses.

3.3 Through time and space

For each family, newly generated from this study and legacy data from previously published studies have been combined to generate a single alignment for the family. The subsequent multi-fasta files were used to create maximum likelihood and date phylogenies. The resulting dated phylogenies were used to reconstruct ancestral ranges.

3.3.1 *Annonaceae*

The *Annonaceae* maximum likelihood (Figure 3.4) and dated (Figure 3.5) phylogenies were generated using 8 target loci – matK, ndhF, rbcL, ycf1, atpB, trnS, trnL, and trnH (Guo et al., 2017). 16 clades (Table 3.1) of *Annonaceae* from this phylogeny were found to be endemic or native to the Western Ghats these are coloured red in figures 3.4 and 3.5. Taxa belong to fourteen different genera that host natives/endemics to the Ghats. The dated tree indicates that *Annonaceae* split away from the rest of the *Magnoliales* approximately 101.35 million years ago (mya). The mega-phylogeny was well resolved with good support values for a majority of the Western Ghats clades unless otherwise specified. *Cyathocalyx zeylanicus* was delimited as clade I, this species is a Western Ghats and Sri Lankan native that found amongst taxa from Continental and Southeast Asia. The minimum node age for clade I was 7.7 million years (myr) with the DEC+J analysis (Figure 3.6) indicating a Continental Asian origin.

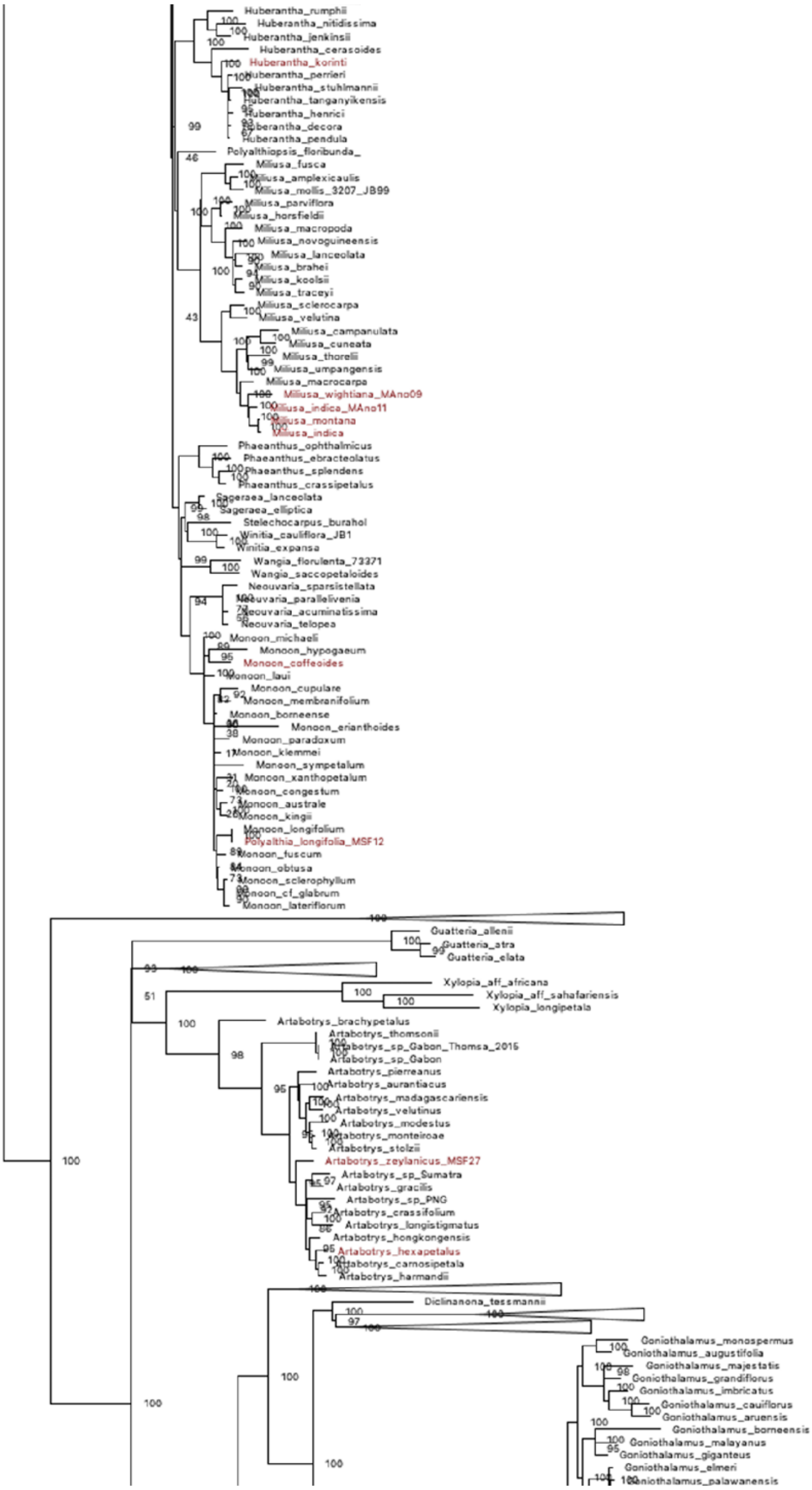
Orophea uniflora (PP 72) a Ghats only endemic that was found amongst taxa from Continental and Southeast Asia formed clade II. The node age for clade II was 7.56 myr and indicated a Sunda Shelf origin. Clade III hosted a Ghats and Sri Lankan native *Huberantha korinti* found between samples from Africa/Madagascar and Continental Asia. The clade had a minimum node age of 14.35 myr and showed likely Continental Asian entry. Clade IV was found amongst taxa from Continental Asia and the Sunda Shelf, it included four species *Miliusa wightiana*, *Miliusa indica_MAno11*, *Miliusa montana*, and *Miliusa indica*. *Miliusa indica* and *Miliusa indica_MAno11* are taxonomically identical but not monophyletic, the species is native to the Western Ghats and Sri Lanka. Clade IV had a minimum node age of 6.64 myr and possibly arrived to the Ghats from Continental Asia. Clade V included *Polyalthia suberosa* it had a minimum node age of 4.09 myr and was sister to taxa from Continental Asia and the Sunda Shelf. This was strongly translated in the DEC+J analysis that indicated a Continental Asian geographic origin.

Clade VI included the sample *Mitrephora heyneana* a Ghats and Sri Lanka native, sister to taxa from the Sunda Shelf. The clade had a minimum node age of 12.29 myr and indicated a strong Sunda Shelf signal. Clade VII consisted of the species *Monoon coffeoides* a Ghats and Sri Lankan endemic, it sat sister to species from Australia and the Sunda Shelf, which was strongly evidenced in the DEC+J analysis that gave it a Sunda Shelf origin. Clade VIII comprised of the species *Monoon longifolium* (PP 81) a Ghats and Sri Lankan native, the species used to be called *Polyalthia longifolia* and was found amongst species from Continental Asia and the Sunda Shelf. The node had a minimum age of 3.4 myr and showed a Sunda Shelf geographic origin. Clade IX was made of *Meiogyne pannosa* a Western Ghats endemic, the taxa was not well supported (PP 42) and found amongst species from New Caledonia and the Sunda and Sahul Shelves. DEC+J analysis gave it a Sahul Shelf entry with a minimum node age of 9.92 myr.

Clade X comprised of the species *Artabotrys zeylanicus* (Western Ghats and Sri Lankan endemic), taxa in the genus are largely from Africa and the Sunda Shelf. The clade had a minimum node of 10.35 myr and showed a Sunda Shelf signal of origin. Clade XI had the species *Artabotrys hexapetalus* found in the Western Ghats, Sri Lanka, and Laos. The species had a minimum node age of 3.33 myr and placed amongst taxa from Continental Asia, which was translated in the DEC+J analysis. Clade XII was the species *Goniothalamus rhynchantherus* (PP 66), a Western Ghats endemic that was not well supported in the phylogeny. It sat amongst samples from Continental Asia and the Sunda Shelf and had a minimum node age of 18.55 myr. DEC+J analysis gave it a Continental Asian origin. Clade XIII was the species *Goniothalamus thwaitesii*, a Western Ghat and Sri Lanka native found amongst species from Sri Lanka. It had a minimum node age of 5.53 myr and showed a Sri Lankan signal of origin.

Clade XIV was made of the Western Ghats endemics *Goniothalamus wightii, Goniothalamus wynaadensis, Goniothalamus cardiopetalus*, it was found sister to taxa from the Sunda Shelf, Sri Lanka and Continental Asia. The clade had a minimum node age of 18.55 million years and showed Continental Asia geographic origin. Clade XV was made of the species *Friesodielsia sahyadrica*, a Western Ghats endemic with a low support value of 69. The taxa sat amongst species from Continental Asia and the Sunda Shelf. DEC+J analysis showed a Continental Asian origin for the clade. It had a minimum node of 11.45 million years. The final *Annonaceae* clade had two species *Uvaria macropoda* and *Uvaria zeylanica* both native of the Western Ghats and Sri Lanka. The clade sat amongst species from Continental Asia, Papua New Guinea and the Sunda Shelf with a minimum node age of 9.01 myr. DEC+J analysis gave the clade a Sri Lankan origin. The DEC+J output from BioGeoBEARS indicated that the family *Annonaceae* may have arrived to the Western Ghats from Continental Asia and the Sunda Shelf. The dated phylogeny indicated that the *Annonaceae* taxa were fairly young arriving between c.3 and 19 million years ago via multiple dispersal events.


OUT_Eupomatia_bennettii
OUT_Liriodendron_tulipifera
OUT_Magnolia_kobus
Meiocarpidium_lepidotum
Lettowianthus_stellatus
Cananga_brandisiana
Cananga_odorata
Drepananthus_petiolatus
Drepananthus_pahangensis
Drepananthus_magnificus
Cyathocalyx_zeylanicus
Cyathocalyx_harmandii
Cyathocalyx_martabanicus
Cyathocalyx_annamensis
Cyathocalyx_sumatranus
Cyathocalyx_magnifructus
Cyathocalyx_globosus
Dendrokingstonia_nervosa
Dendrokingstonia_gardnerii
Mitrephora_heyneana_MAno13
Mitrephora_vittata
Mitrephora_celebica
Mitrephora_maingayi
Mitrephora_alba
Mitrephora_keithii
Mitrephora_polypyrena
Mitrephora_tomentosa
Platymitra_sp_TC2012
Platymitra_macrocarpa
Alphonsea_javanica
Alphonsea_kinabaluensis
Alphonsea_johorensis
Alphonsea_elliptica
Alphonsea_hainanensis
Alphonsea_glandulosa
Alphonsea_monogyna
Alphonsea_mollis
Alphonsea_boniana
Meiogyne_hainanensis
Meiogyne_virgata
Meiogyne_mindorensis
Meiogyne_pannosa
Meiogyne_monosperma
Meiogyne_sp2_Indu2457
Meiogyne_sp_TNW_146
Meiogyne_baillonii
Meiogyne_glabra
Meiogyne_lecardii
Meiogyne_amicorum
Meiogyne_habrotricha
Meiogyne_amygdalina
Meiogyne_stenopetala_subsp_insularis
Meiogyne_laddiana
Meiogyne_dumetosa
Meiogyne_cylindrocarpa_Guam
Meiogyne_verrucosa
Meiogyne_trichocarpa_2
Meiogyne_trichocarpa_1
Meiogyne_heteropetala
Meiogyne_bidwillii
Meiogyne_stenopetala
Meiogyne_hirsuta
Wuodendron_praecox_XB190
Wuodendron_litseifolium
Orophea_polycarpa
Orophea_uniflora_MAno04
Orophea_cf_laui
Orophea_creaghii
Orophea_kerrii
Orophea_enterocarpa
Orophea_brandisii
Orophea_celebica
Orophea_enneandra
Orophea_cuneiformis
Popowia_pisocarpa
Popowia_fusca
Popowia_odoardi
Popowia_hirta
Polyalthia_stenopetala
Polyalthia_debilis
Polyalthia_evecta
Polyalthia_parviflora
Polyalthia_motleyana
Polyalthia_kanchanaburiana
Polyalthia_suberosa
Polyalthia_suberosa_MAno07
Polyalthia_lateritia
Polyalthia_subcordata
Polyalthia_cinnamomea
Polyalthia_cf_miliusoides
Polyalthia_hispida
Polyalthia_xanthocarpa
Polyalthia_longirostris
Polyalthia_lanceolata
Polyalthia_bullata
Polyalthia_borneensis
Polyalthia_obliqua
Polyalthia_celebica
Polyalthia_insignis
Polyalthia_submontana
Polyalthia_johnsonii
Polyalthia_trochilia
Polyalthia_cf_subsessilifolia
Polyalthia_cauliflora
Polyalthia_flagellaris
Polyalthia_angustissima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Huberantha_tanganyikensis
Huberantha_henrici
Huberantha_decora
Huberantha_pendula
Polyalthiopsis_floribunda_
Miliusa_fusca
Miliusa_amplexicaulis
Miliusa_mollis_3207_JB99
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Miliusa_horsfieldii
Miliusa_macropoda
Miliusa_novoguineensis
Miliusa_lanceolata
Miliusa_brahei
Miliusa_koolsii
Miliusa_traceyi
Miliusa_sclerocarpa
Miliusa_velutina
Miliusa_campanulata
Miliusa_cuneata
Miliusa_thorelii
Miliusa_umpangensis
Miliusa_macrocarpa
Miliusa_wightiana_MAno09
Miliusa_indica_MAno11
Miliusa_montana
Miliusa_indica
Phaeanthus_ophthalmicus
Phaeanthus_ebracteolatus
Phaeanthus_splendens
Phaeanthus_crassipetalus
Sageraea_lanceolata
Sageraea_elliptica
Stelechocarpus_burahol
Winitia_cauliflora_JB1
Winitia_expansa
Wangia_florulenta_73371
Wangia_saccopetaloides
Neouvaria_sparsistellata
Neouvaria_parallelivenia
Neouvaria_acuminatissima
Neouvaria_telopea
Monoon_michaeli
Monoon_hypogaeum
Monoon_coffeoides
Monoon_laui
Monoon_cupulare
Monoon_membranifolium
Monoon_borneense
Monoon_erianthoides
Monoon_paradoxum
Monoon_klemmei
Monoon_sympetalum
Monoon_xanthopetalum
Monoon_congestum
Monoon_australe
Monoon_kingii
Monoon_longifolium
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Monoon_fuscum
Monoon_obtusa
Monoon_sclerophyllum
Monoon_cf_glabrum
Monoon_lateriflorum
Guatteria_allenii
Guatteria_atra
Guatteria_elata
Xylopia_aff_africana
Xylopia_aff_sahafariensis
Xylopia_longipetala
Artabotrys_brachypetalus
Artabotrys_thomsonii
Artabotrys_sp_Gabon_Thomsa_2015
Artabotrys_sp_Gabon
Artabotrys_pierreanus
Artabotrys_aurantiacus
Artabotrys_madagascariensis
Artabotrys_velutinus
Artabotrys_modestus
Artabotrys_monteiroae
Artabotrys_stolzii
Artabotrys_zeylanicus_MSF27
Artabotrys_sp_Sumatra
Artabotrys_gracilis
Artabotrys_sp_PNG
Artabotrys_crassifolium
Artabotrys_longistigmatus
Artabotrys_hongkongensis
Artabotrys_hexapetalus
Artabotrys_carnosipetala
Artabotrys_harmandii
Diclinanona_tessmannii
Goniothalamus_monospermus
Goniothalamus_augustifolia
Goniothalamus_majestatis
Goniothalamus_grandiflorus
Goniothalamus_imbricatus
Goniothalamus_cauiflorus
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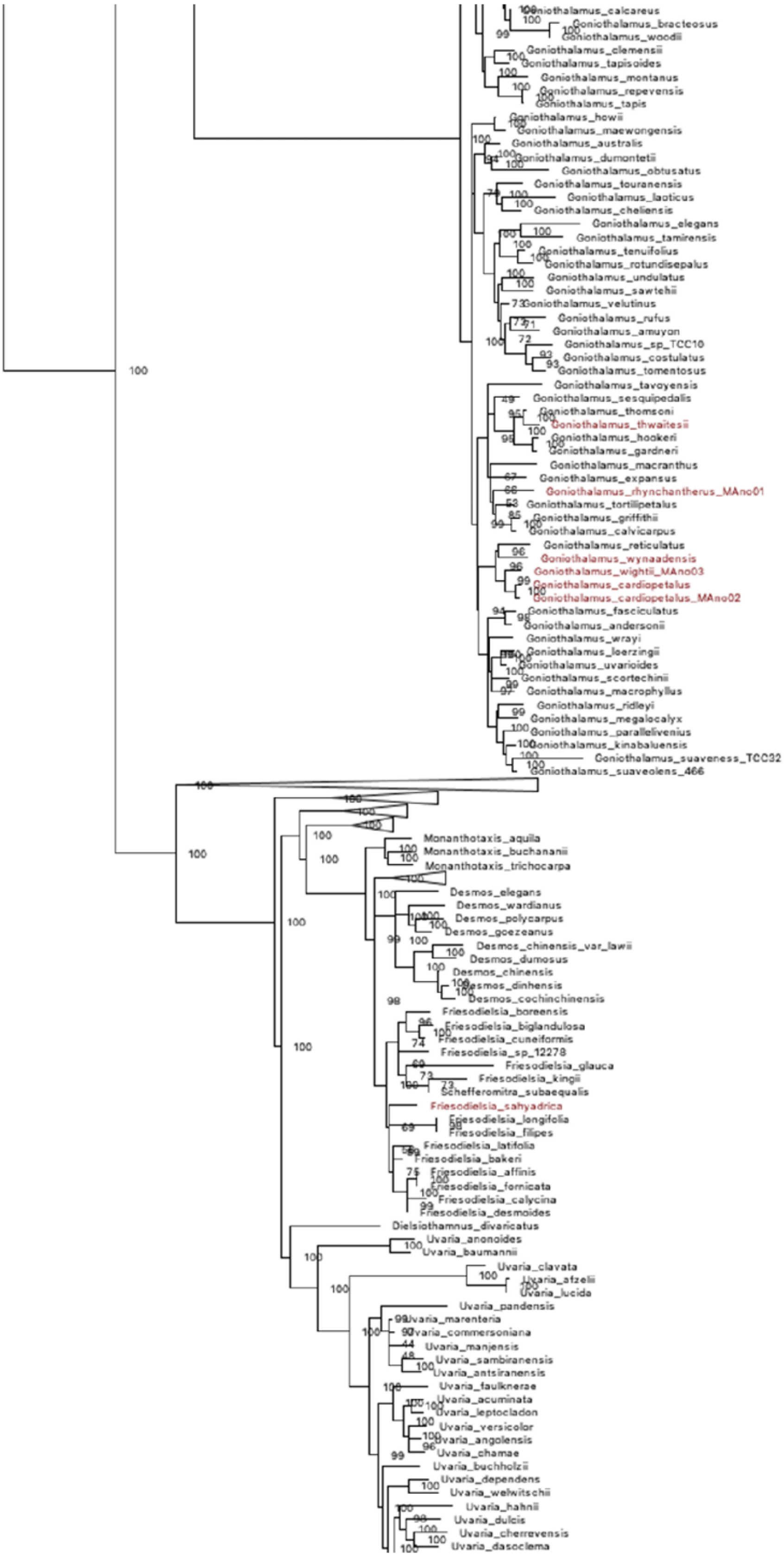
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Goniothalamus_bracteosus
Goniothalamus_woodii
Goniothalamus_clemensii
Goniothalamus_tapisoides
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Goniothalamus_repevensis
Goniothalamus_tapis
Goniothalamus_howii
Goniothalamus_maewongensis
Goniothalamus_australis
Goniothalamus_dumontetii
Goniothalamus_obtusatus
Goniothalamus_touranensis
Goniothalamus_laoticus
Goniothalamus_cheliensis
Goniothalamus_elegans
Goniothalamus_tamirensis
Goniothalamus_tenuifolius
Goniothalamus_rotundisepalus
Goniothalamus_undulatus
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Goniothalamus_velutinus
Goniothalamus_rufus
Goniothalamus_amuyon
Goniothalamus_sp_TCC10
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Goniothalamus_tomentosus
Goniothalamus_tavoyensis
Goniothalamus_sesquipedalis
Goniothalamus_thomsoni
Goniothalamus_thwaitesii
Goniothalamus_hookeri
Goniothalamus_gardneri
Goniothalamus_macranthus
Goniothalamus_expansus
Goniothalamus_rhynchantherus_MAno01
Goniothalamus_tortilipetalus
Goniothalamus_griffithii
Goniothalamus_calvicarpus
Goniothalamus_reticulatus
Goniothalamus_wynaadensis
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Goniothalamus_cardiopetalus
Goniothalamus_cardiopetalus_MAno02
Goniothalamus_fasciculatus
Goniothalamus_andersonii
Goniothalamus_wrayi
Goniothalamus_loerzingii
Goniothalamus_uvarioides
Goniothalamus_scortechinii
Goniothalamus_macrophyllus
Goniothalamus_ridleyi
Goniothalamus_megalocalyx
Goniothalamus_parallelivenius
Goniothalamus_kinabaluensis
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Monanthotaxis_aquila
Monanthotaxis_buchananii
Monanthotaxis_trichocarpa
Desmos_elegans
Desmos_wardianus
Desmos_polycarpus
Desmos_goezeanus
Desmos_chinensis_var_lawii
Desmos_dumosus
Desmos_chinensis
Desmos_dinhensis
Desmos_cochinchinensis
Friesodielsia_boreensis
Friesodielsia_biglandulosa
Friesodielsia_cuneiformis
Friesodielsia_sp_12278
Friesodielsia_glauca
Friesodielsia_kingii
Schefferomitra_subaequalis
Friesodielsia_sahyadrica
Friesodielsia_longifolia
Friesodielsia_filipes
Friesodielsia_latifolia
Friesodielsia_bakeri
Friesodielsia_affinis
Friesodielsia_fornicata
Friesodielsia_calycina
Friesodielsia_desmoides
Dielsiothamnus_divaricatus
Uvaria_anonoides
Uvaria_baumannii
Uvaria_clavata
Uvaria_afzelii
Uvaria_lucida
Uvaria_pandensis
Uvaria_marenteria
Uvaria_commersoniana
Uvaria_manjensis
Uvaria_sambiranensis
Uvaria_antsiranensis
Uvaria_faulknerae
Uvaria_acuminata
Uvaria_leptocladon
Uvaria_versicolor
Uvaria_angolensis
Uvaria_chamae
Uvaria_buchholzii
Uvaria_dependens
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Uvaria_hahnii
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Uvaria_cherrevensis
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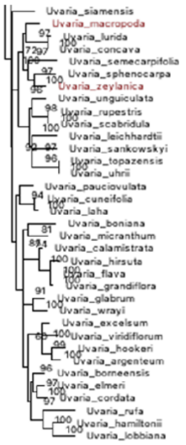
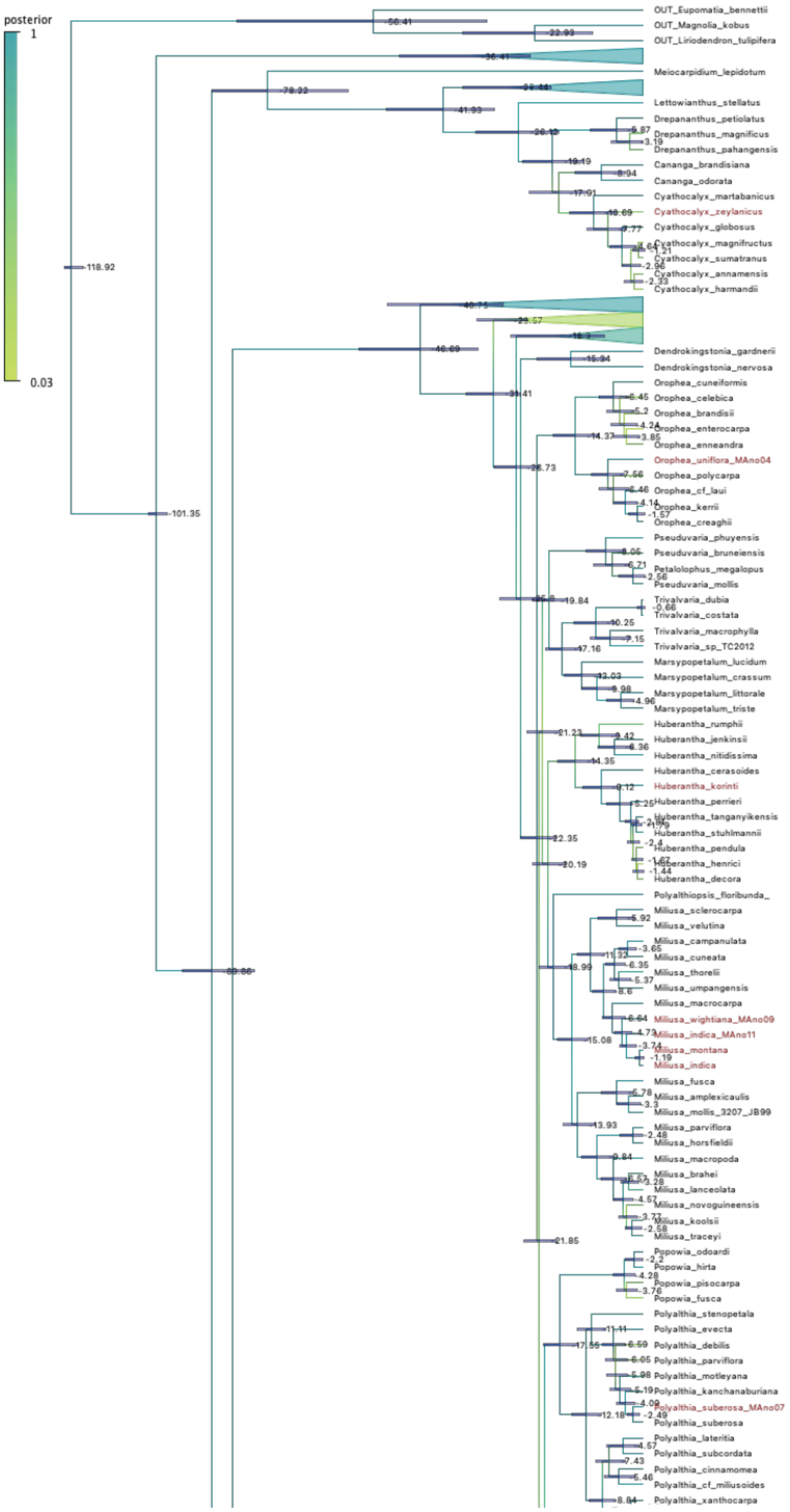


Figure 3.4: Maximum Likelihood tree for the family *Annonaceae*.

The tree was generated in IQTREE using the loci matK, ndhF, rbcL, ycf1, atpB, trnS, trnL, and trnH for 630 taxa. Samples in red indicate taxa that are native or endemic to the Western Ghats. Numbers on the nodes depict posterior probability values for the clades. Collapsed branches are clades that hosted no taxa from the Western Ghats.


posterior
1
0.03
118.92
101.35
56.41
22.93
36.41
78.22
41.93
28.44
26.12
5.87
3.19
19.49
8.94
17.91
10.69
7.77
1.21
2.96
2.33
40.75
29.57
19.3
46.69
15.84
31.41
26.73
6.45
5.2
4.24
3.85
14.37
7.56
6.46
4.14
1.57
8.06
6.71
2.56
19.84
0.66
10.25
7.15
17.16
13.03
8.98
4.96
21.23
9.42
6.36
14.35
9.12
5.25
1.79
2.4
1.67
1.44
22.35
20.19
5.92
3.65
11.32
6.35
5.37
8.6
18.99
6.64
4.73
3.74
1.19
15.08
6.78
3.3
13.93
2.48
9.84
3.28
4.57
3.77
2.58
21.85
2.2
4.28
3.76
11.11
17.55
6.59
6.05
5.98
5.19
4.09
2.49
12.18
4.57
7.43
5.46
8.84
83.86
OUT_Eupomatia_bennettii
OUT_Magnolia_kobus
OUT_Liriodendron_tulipifera
Meiocarpidium_lepidotum
Lettowianthus_stellatus
Drepananthus_petiolatus
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Orophea_kerrii
Orophea_creaghii
Pseuduvaria_phuyensis
Pseuduvaria_bruneiensis
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Pseuduvaria_mollis
Trivalvaria_dubia
Trivalvaria_costata
Trivalvaria_macrophylla
Trivalvaria_sp_TC2012
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Marsypopetalum_crassum
Marsypopetalum_littorale
Marsypopetalum_triste
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Huberantha_cerasoides
Huberantha_korinti
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Huberantha_tanganyikensis
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Polyalthiopsis_floribunda_
Miliusa_sclerocarpa
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Miliusa_horsfieldii
Miliusa_macropoda
Miliusa_brahei
Miliusa_lanceolata
Miliusa_novoguineensis
Miliusa_koolsii
Miliusa_traceyi
Popowia_odoardi
Popowia_hirta
Popowia_pisocarpa
Popowia_fusca
Polyalthia_stenopetala
Polyalthia_evecta
Polyalthia_debilis
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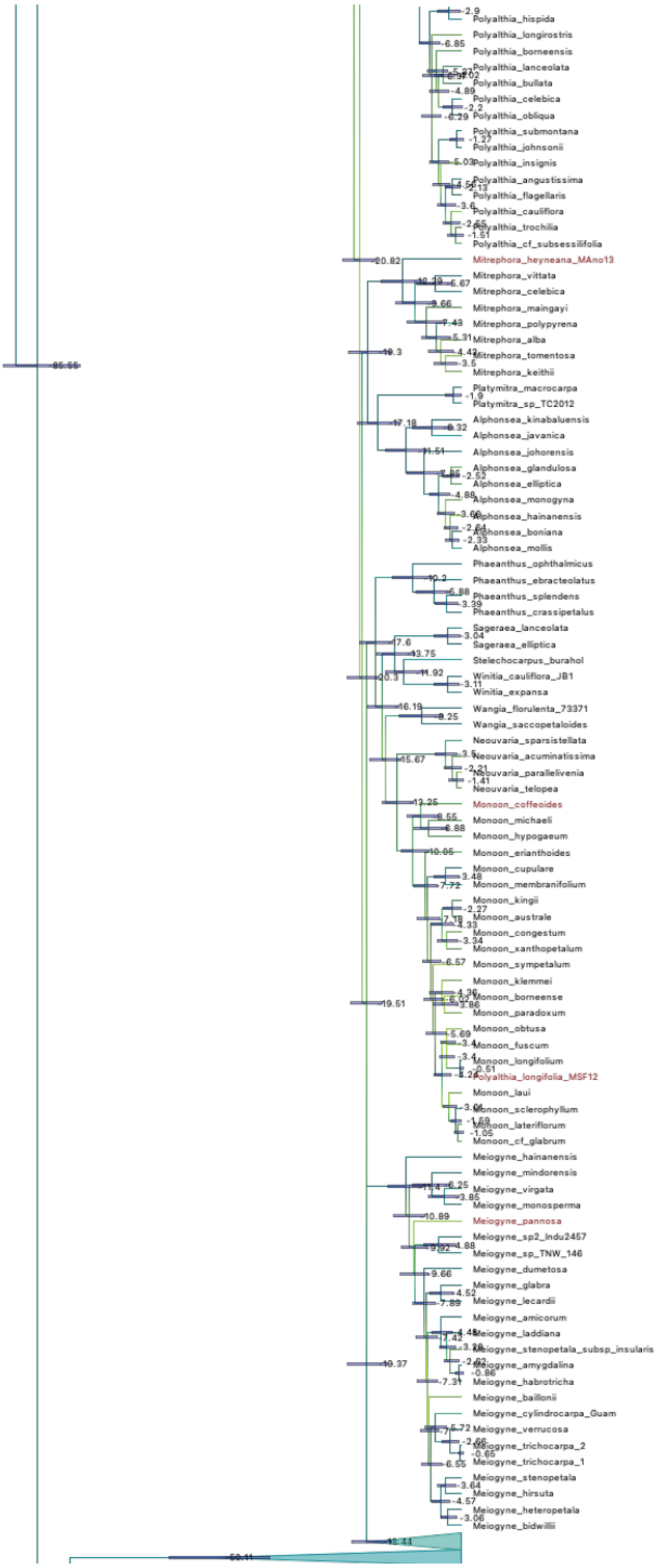
2.9
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Polyalthia_longirostris
6.85
Polyalthia_borneensis
Polyalthia_lanceolata
Polyalthia_bullata
4.89
Polyalthia_celebica
2.2
6.29
Polyalthia_obliqua
Polyalthia_submontana
1.27
Polyalthia_johnsonii
5.03
Polyalthia_insignis
Polyalthia_angustissima
2.13
Polyalthia_flagellaris
3.6
Polyalthia_cauliflora
Polyalthia_trochilia
1.51
Polyalthia_cf_subsessilifolia
20.82
Mitrephora_heyneana_MAno13
Mitrephora_vittata
6.67
Mitrephora_celebica
9.66
Mitrephora_maingayi
7.43
Mitrephora_polypyrena
5.31
Mitrephora_alba
4.42
Mitrephora_tomentosa
3.5
Mitrephora_keithii
85.55
Platymitra_macrocarpa
1.9
Platymitra_sp_TC2012
17.18
Alphonsea_kinabaluensis
8.32
Alphonsea_javanica
11.51
Alphonsea_johorensis
Alphonsea_glandulosa
2.52
Alphonsea_elliptica
4.88
Alphonsea_monogyna
Alphonsea_hainanensis
Alphonsea_boniana
2.33
Alphonsea_mollis
Phaeanthus_ophthalmicus
10.2
Phaeanthus_ebracteolatus
5.88
Phaeanthus_splendens
3.39
Phaeanthus_crassipetalus
Sageraea_lanceolata
3.04
Sageraea_elliptica
17.6
13.75
Stelechocarpus_burahol
20.3
11.92
Winitia_cauliflora_JB1
3.11
Winitia_expansa
16.19
Wangia_florulenta_73371
8.25
Wangia_saccopetaloides
Neouvaria_sparsistellata
Neouvaria_acuminatissima
15.67
2.21
Neouvaria_parallelivenia
1.41
Neouvaria_telopea
13.25
Monoon_coffeoides
8.55
Monoon_michaeli
6.88
Monoon_hypogaeum
10.05
Monoon_erianthoides
Monoon_cupulare
3.48
7.72
Monoon_membranifolium
Monoon_kingii
2.27
Monoon_australe
4.33
Monoon_congestum
3.34
Monoon_xanthopetalum
6.57
Monoon_sympetalum
Monoon_klemmei
4.36
Monoon_borneense
3.86
19.51
Monoon_paradoxum
Monoon_obtusa
5.69
3.4
Monoon_fuscum
3.4
Monoon_longifolium
0.51
Polyalthia_longifolia_MSF12
Monoon_laui
Monoon_sclerophyllum
Monoon_lateriflorum
1.05
Monoon_cf_glabrum
Meiogyne_hainanensis
Meiogyne_mindorensis
6.25
Meiogyne_virgata
3.85
Meiogyne_monosperma
10.89
Meiogyne_pannosa
Meiogyne_sp2_Indu2457
9.92
4.88
Meiogyne_sp_TNW_146
Meiogyne_dumetosa
9.66
Meiogyne_glabra
4.52
7.89
Meiogyne_lecardii
Meiogyne_amicorum
Meiogyne_laddiana
7.42
Meiogyne_stenopetala_subsp_insularis
Meiogyne_amygdalina
19.37
0.86
7.31
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Meiogyne_trichocarpa_1
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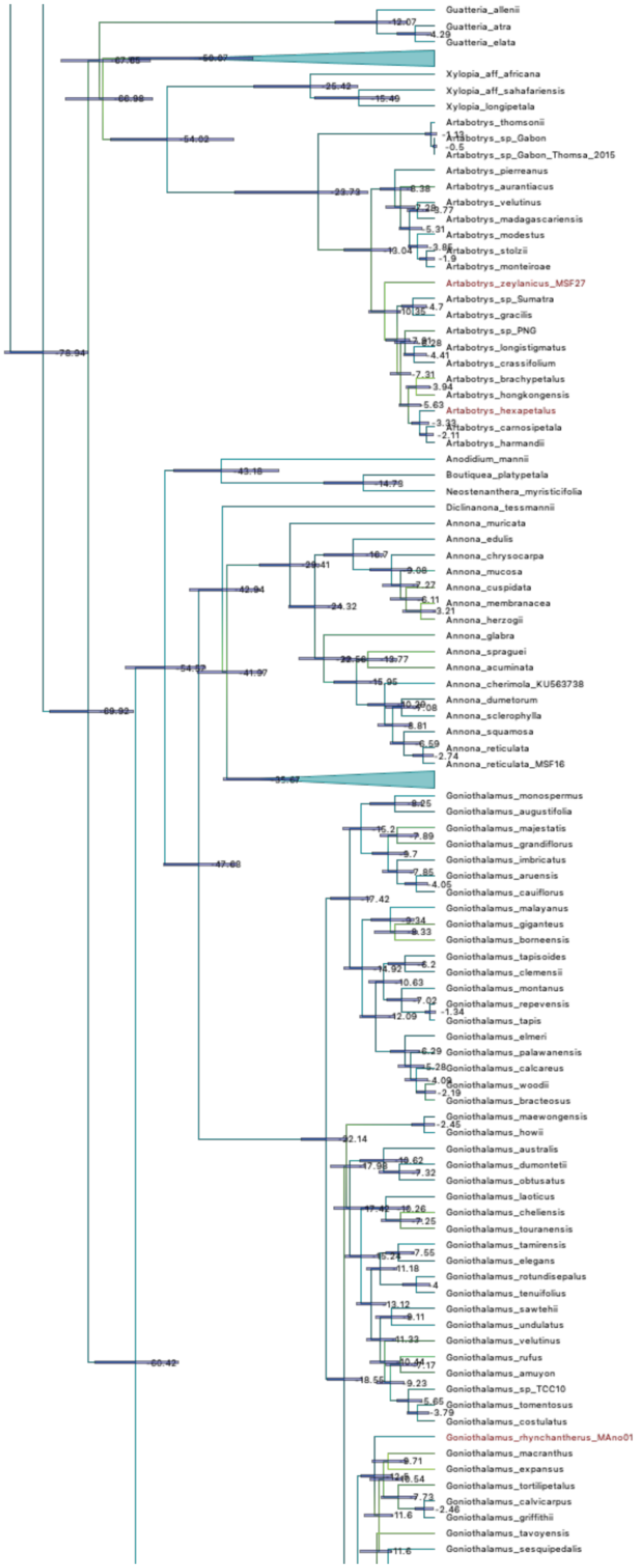
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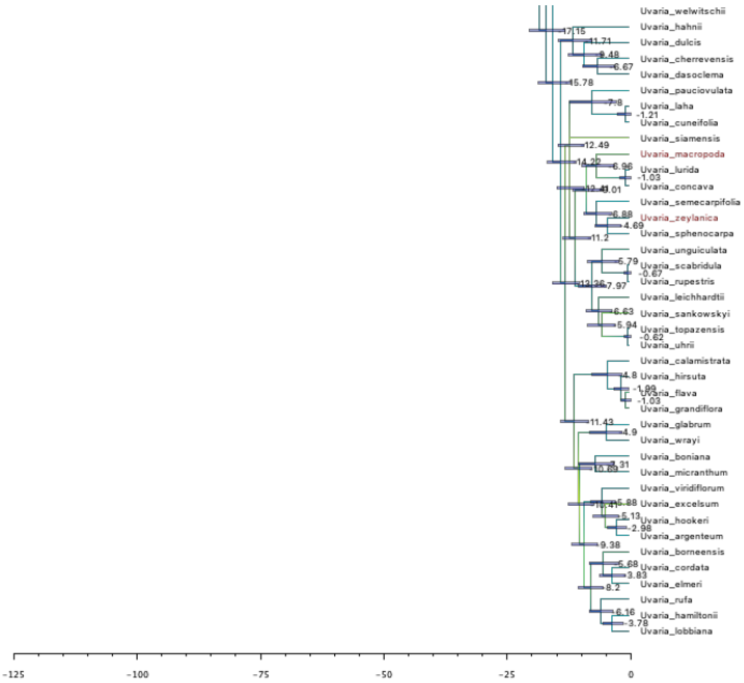
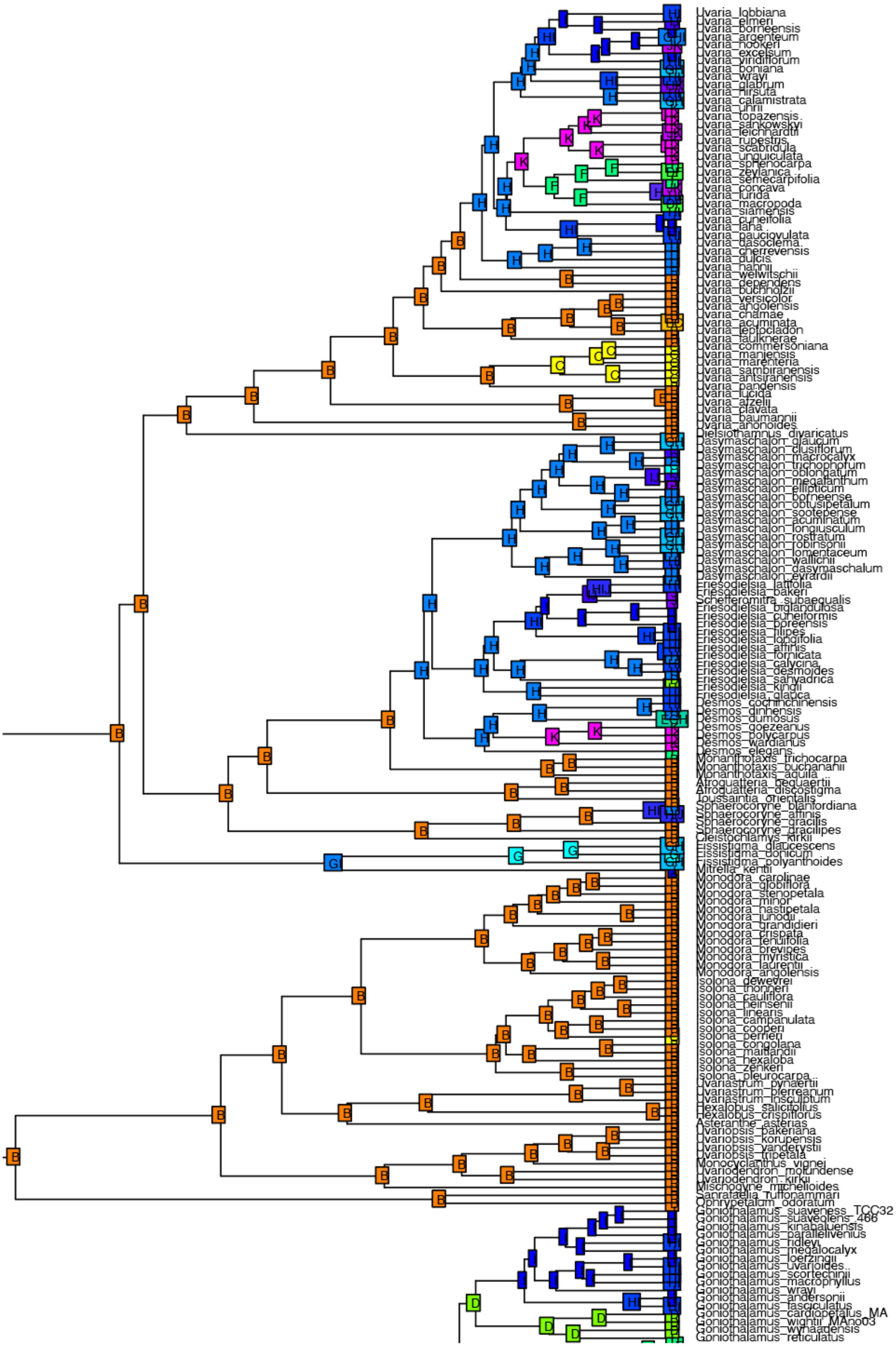


Figure 3.5: Time calibrated phylogeny of the family *Annonaceae* for 630 taxa.

Samples in red indicate taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest. Collapsed branches are clades that hosted no taxa from the Western Ghats.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Uvaria_topazensis
Uvaria_sankowskyi
Uvaria_leichhardtii
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Uvaria_sphenocarpa
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Uvaria_siamensis
Uvaria_cuneifolia
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Uvaria_dasoclema
Uvaria_cherrevensis
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Uvaria_welwitschii
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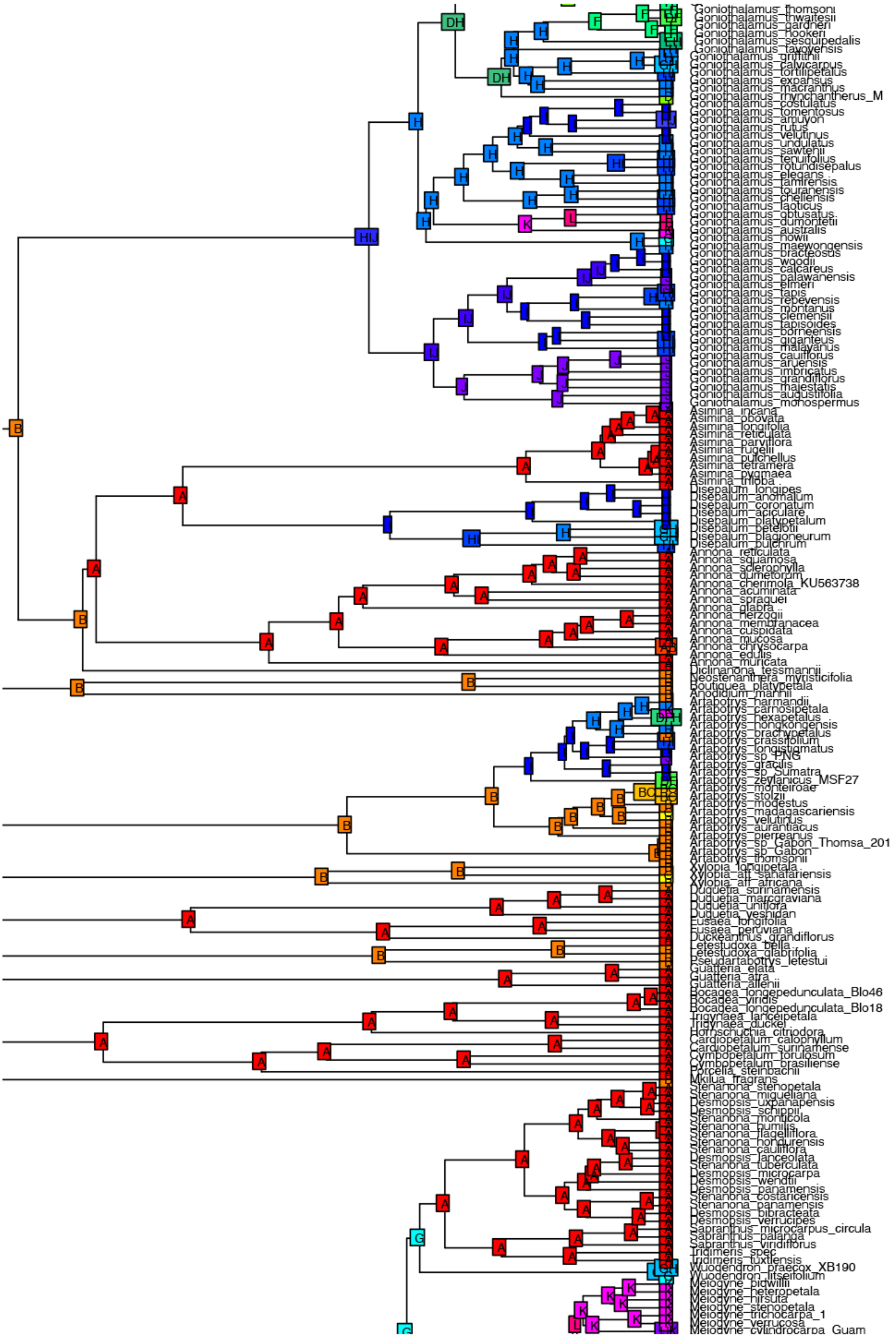
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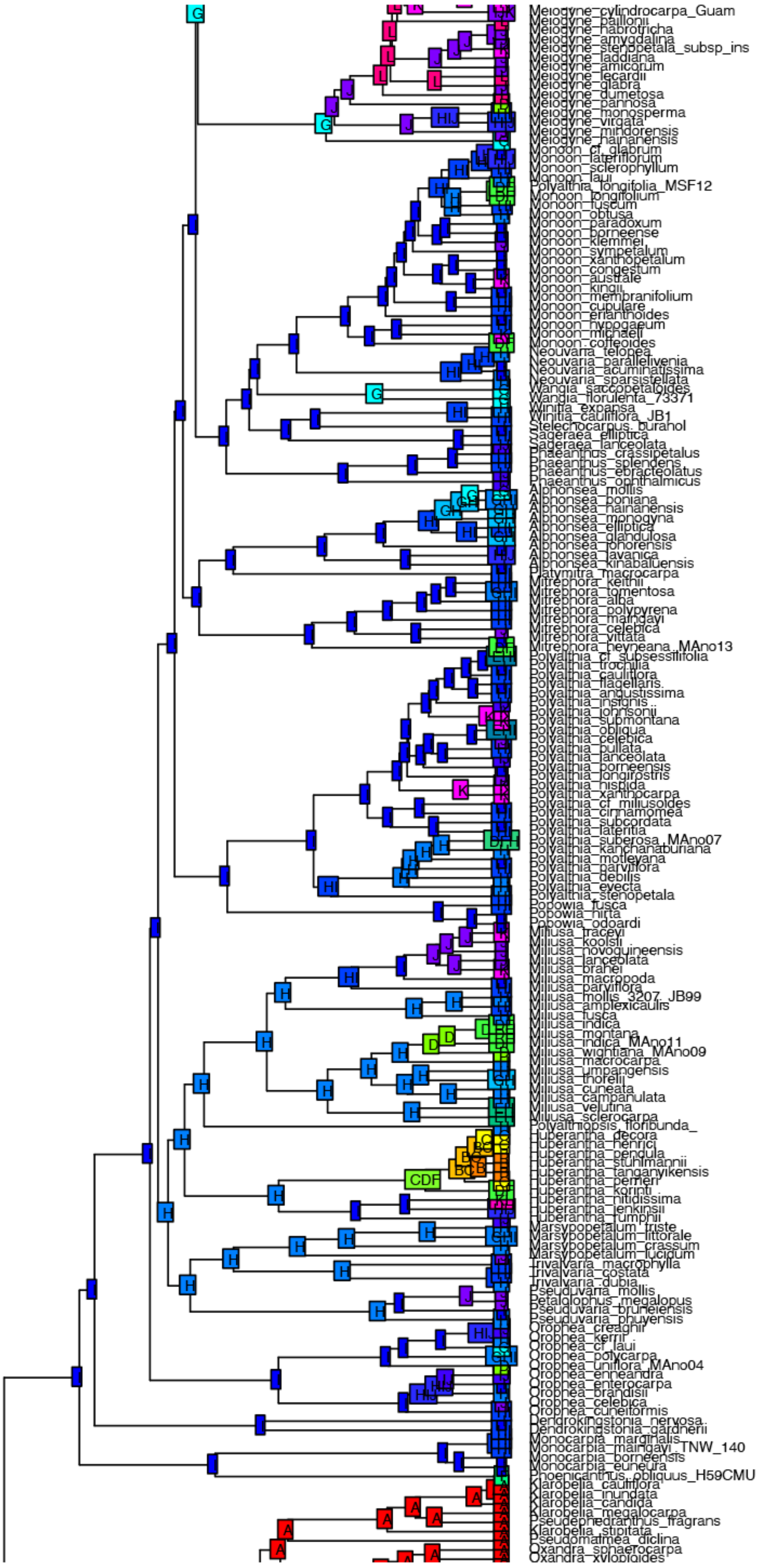
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Miliusa_campanulata
Miliusa_velutina
Miliusa_sclerocarpa
Polyalthiopsis_floribunda_
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Huberantha_henrici
Huberantha_pendula
Huberantha_stuhlmannii
Huberantha_tanganyikensis
Huberantha_perrieri
Huberantha_korinti
Huberantha_nitidissima
Huberantha_jenkinsii
Huberantha_rumphii
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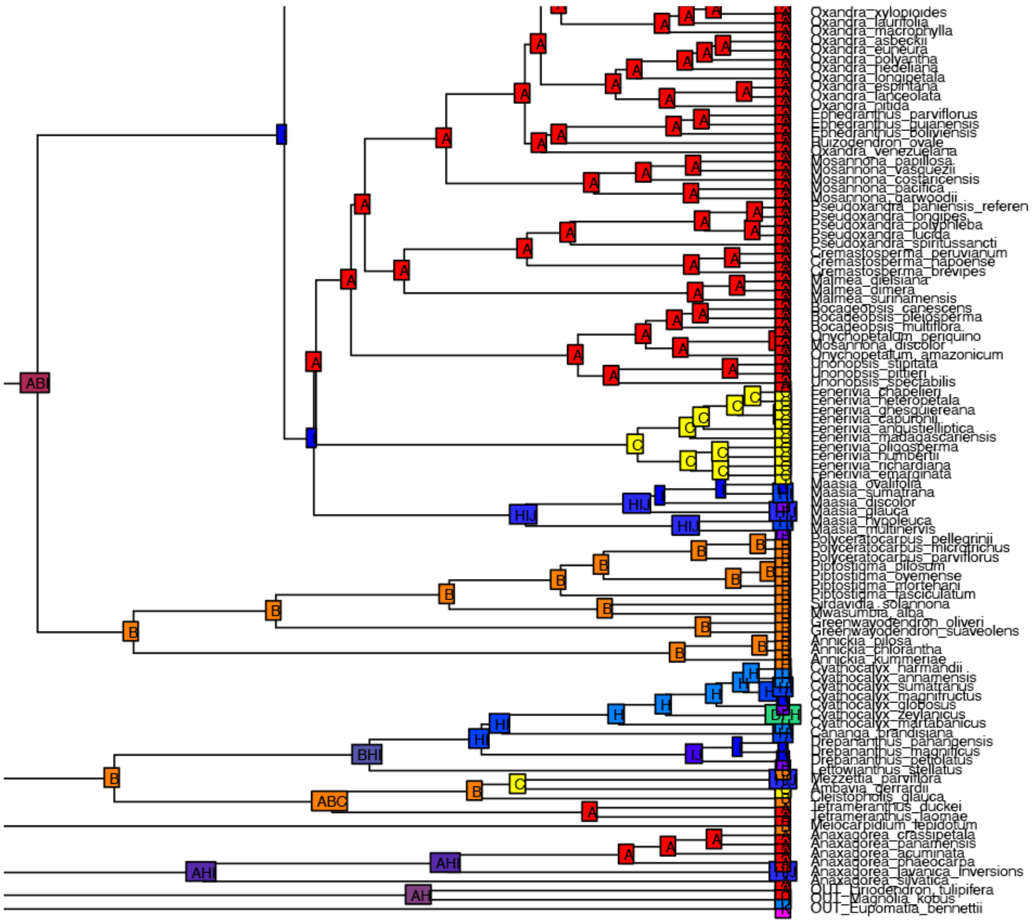


Figure 3.6: DEC+J ancestral area reconstruction for the family *Annonaceae*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Western Ghats (Light green), E=Himalayas (Green), F=Sri Lanka (Neon green), G=China (Light blue), H=Continental Asia (Indigo), I=Sunda Shelf (Royal blue), J=Sahul Shelf (Purple), K=PNG (Magenta), L=Philippines (Pink). DEC+ J analysis had LnL value of -1444. Clades listed in Table 3.1

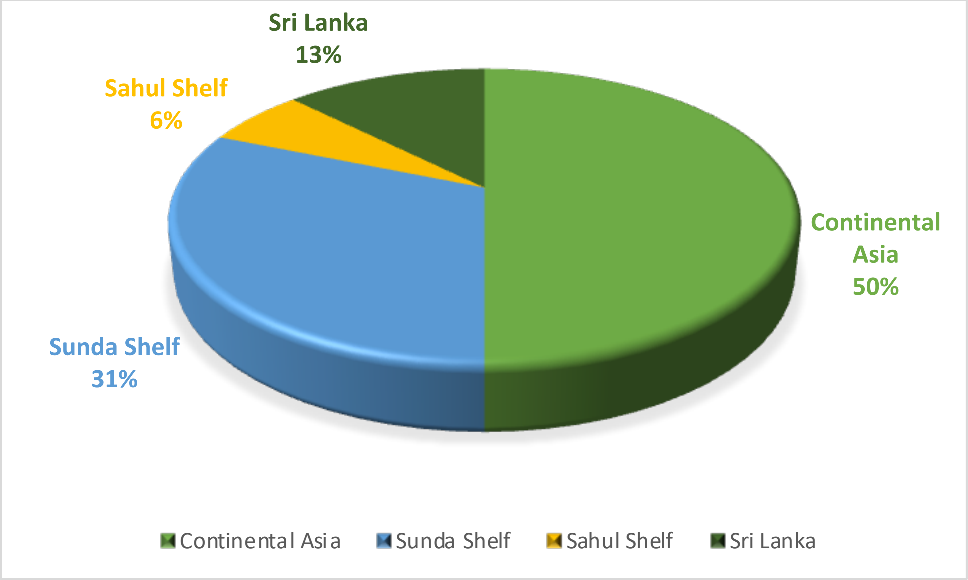


Figure 3.7: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Annonaceae*.

Event	**Taxa in the event**	**Minimum Age (mya)**	**Area Code**
Annonaceae I	*Cyathocalyx zeylanicus*	7.7	H
Annonaceae II	*Orophea uniflora MAno04*	7.56	I
Annonaceae III	*Huberantha korinti*	14.35	H
Annonaceae IV	*Miliusa wightiana MAno09, Miliusa indica MAno11, Miliusa montana and Milusa indica*	6.64	H
Annonaceae V	*Polyalthia suberosa MAno07*	4.09	H
Annonaceae VI	*Mitrephora heyneana MAno13*	12.29	I
Annonaceae VII	*Monoon coffeoides*	8.55	I
Annonaceea VIII	*Monoon longifolium*	3.4	I
Annonaceae IX	*Meiogyne pannosa*	9.92	J
Annonaceae X	*Artabotrys zeylanicus MSF27*	10.35	I
Annonaceae XI	*Artabotrys hexapetalus*	3.33	H
Annonaceae XII	*Goniothalamus rhynchantherus MAno01*	18.55	H
Annonaceae XIII	*Goniothalamus thwaitesii*	5.53	F
Annonaceae XIV	*Goniothalamus wightii MAno03, Goniothalamus wynaadensis, Goniothalamus cardiopetalus MAno02*	18.55	H
Annonaceae XV	*Friesodielsia sahyadrica*	11.45	H
Annonaceae XVI	*Uvaria macropoda, Uvaria zeylanica*	9.01	F

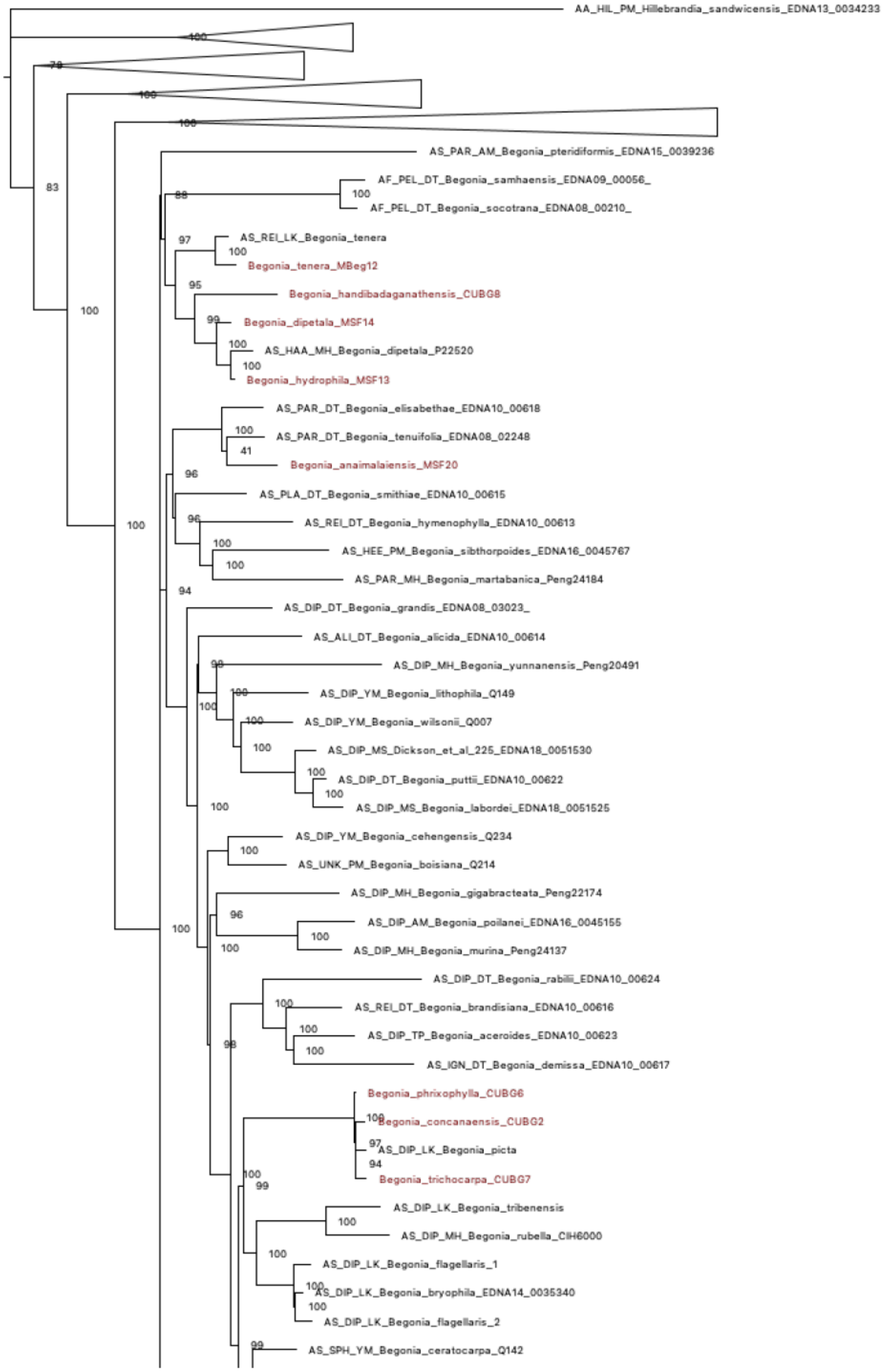
Table 3.1: *Annonaceae* table showing clade number, taxa found in each clade, their minimum age, and geographic origin.

3.3.2 *Begoniaceae*

The maximum likelihood (Figure 3.8) and time calibrated (Figure 3.9) phylogenies of *Begoniaceae* were generated using three target loci – nadh, ndhF and trnL (Moonlight et al., 2018). Four clades (Table 3.2) were found endemic to the Western Ghats. Samples in red in the ML and dated phylogenies are taxa native to the Ghats. The dated tree shows the *Begonia* split away from the monophyletic genus *Hillebrandia* approximately 24 mya. The analyses have ten taxa that are found in the Western Ghats. Clade I hosted the sample *Begonia anaimalaiensis*, a Western Ghats endemic that sits amongst samples from Continental Asia and the Sunda Shelf. The clade was not well supported (PP 41), it had a minimum node of 3.13 myr and a Sunda Shelf signal of geographic origin. Clade II consisted of three taxa – *Begonia trichocarpa*, *Begonia phrixophylla*, and *Begonia concanensis*. *Begonia concanensis and Begonia phrixophylla* are Western Ghats endemics while *Begonia trichocarpa* is native to both the Ghats and the Himalayas. The clade is well resolved and had a minimum node age of 7.45 myr and showed a Himalayan signal for geographic origin in the DEC+J analysis (Figure 3.10).

Clade III had four taxa – *Begonia tenera*, *Begonia dipetala*, *Begonia hydrophila*, and *Begonia handibadaganathensis*. *Begonia tenera* is a Ghats and Sri Lankan native. *Begonia dipetala*, *Begonia handibadaganathensis*, and *Begonia hydrophila* are Western Ghats endemics. *Begonia hydrophila* is not sister to *Begonia malabarica* as current taxonomy would suggest. The taxa sit amongst samples from Socotra, the Himalayas and Sri Lanka. The Socotra clade was not well supported (PP 88). Clade III was well supported with a minimum node of 13.05 myr and arrived to the Western Ghats from Continental Asia. Clade IV consisted of the taxa *Begonia malabarica* and *Begonia fallax*. The clade itself was well supported but the placement of *Begonia fallax* (PP 82) as sister to *Begonia malabarica* was not. The clade sat amongst taxa from Sri Lanka, Continental Asia, and the Sunda Shelf, had a minimum node age of 12.65 myr, and showed signal from China. The time calibrated *Begoniaceae* phylogeny indicated that *Begonias* arrived to the Western Ghats between c.3 and 13 million years ago. All four clades had a different geographic origin signal – the Himalayas, Sri Lanka, Continental Asia, and China. Each area of origin held equal weight.

Taxonomically *Begonia malabarica, Begonia dipetala, Begonia hydrophila*, and *Begonia fallax* have been lumped together under two names – *Begonia malabarica* and *Begonia dipetala.* From morphology alone it is quite visible that these are four distinct species. Each of them has distinct characteristics that give them their individual species concepts. This difference is also depicted in the molecular phylogenies. In the final phylogeny the names *Begonia hydrophila* and *Begonia fallax* have been resurrected and used alongside *Begonia dipetala* and *Begonia malabarica* as taxonomic placeholders. The taxonomic clarification of the cane *Begonia*s of the Western Ghats is a work in progress and beyond the scope of this thesis.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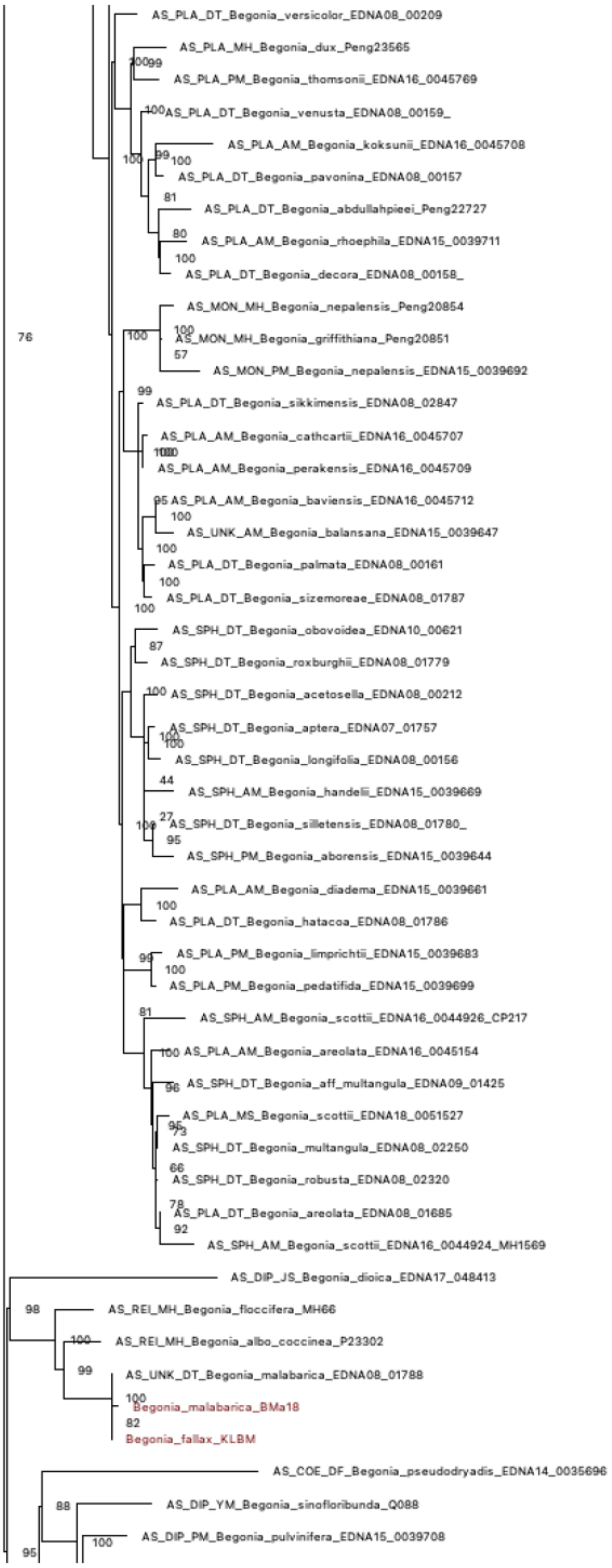
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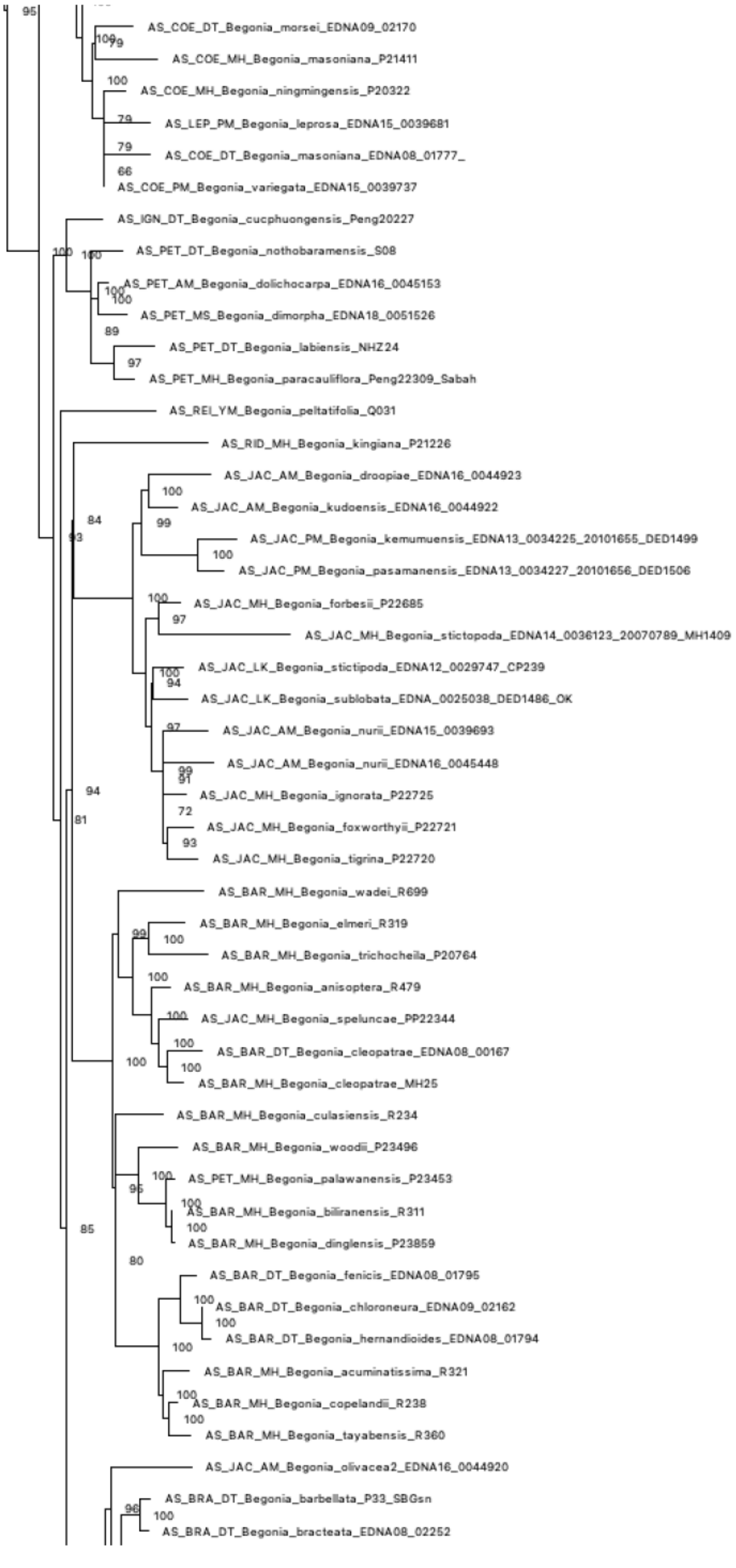
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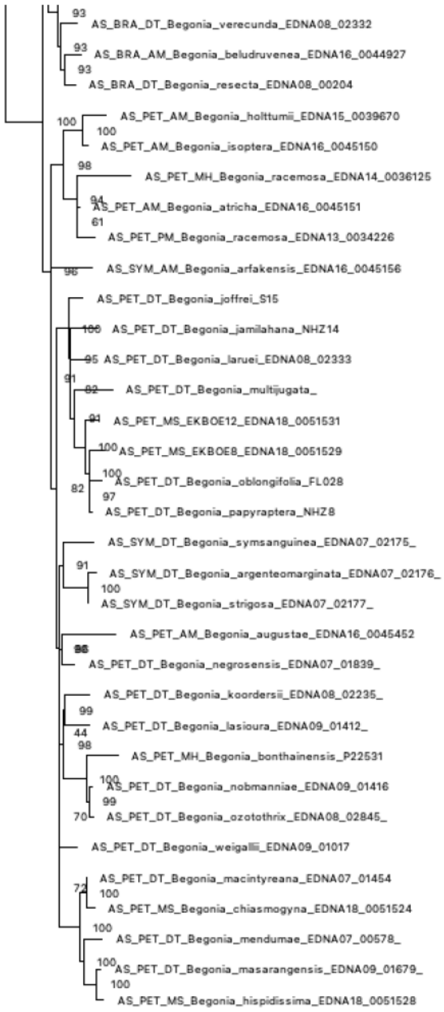
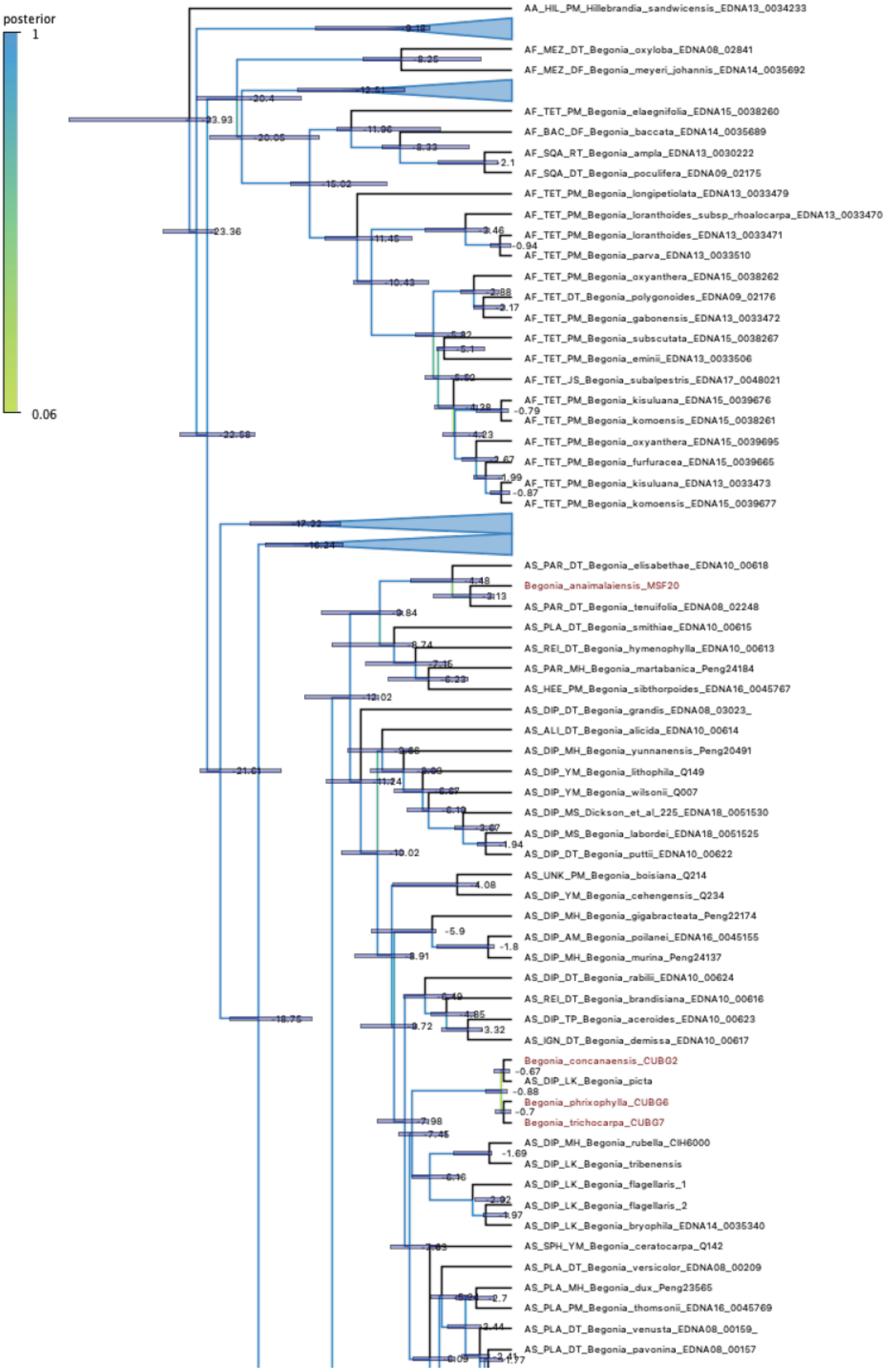


Figure 3.8: Maximum Likelihood tree for the family Begoniaceae.

The maximum likelihood phylogeny was generated for 372 taxa using IQTREE for the target loci nadh, ndhF, and trnL. Samples in red indicate taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades. Collapsed branches are clades that hosted no taxa from the Western Ghats.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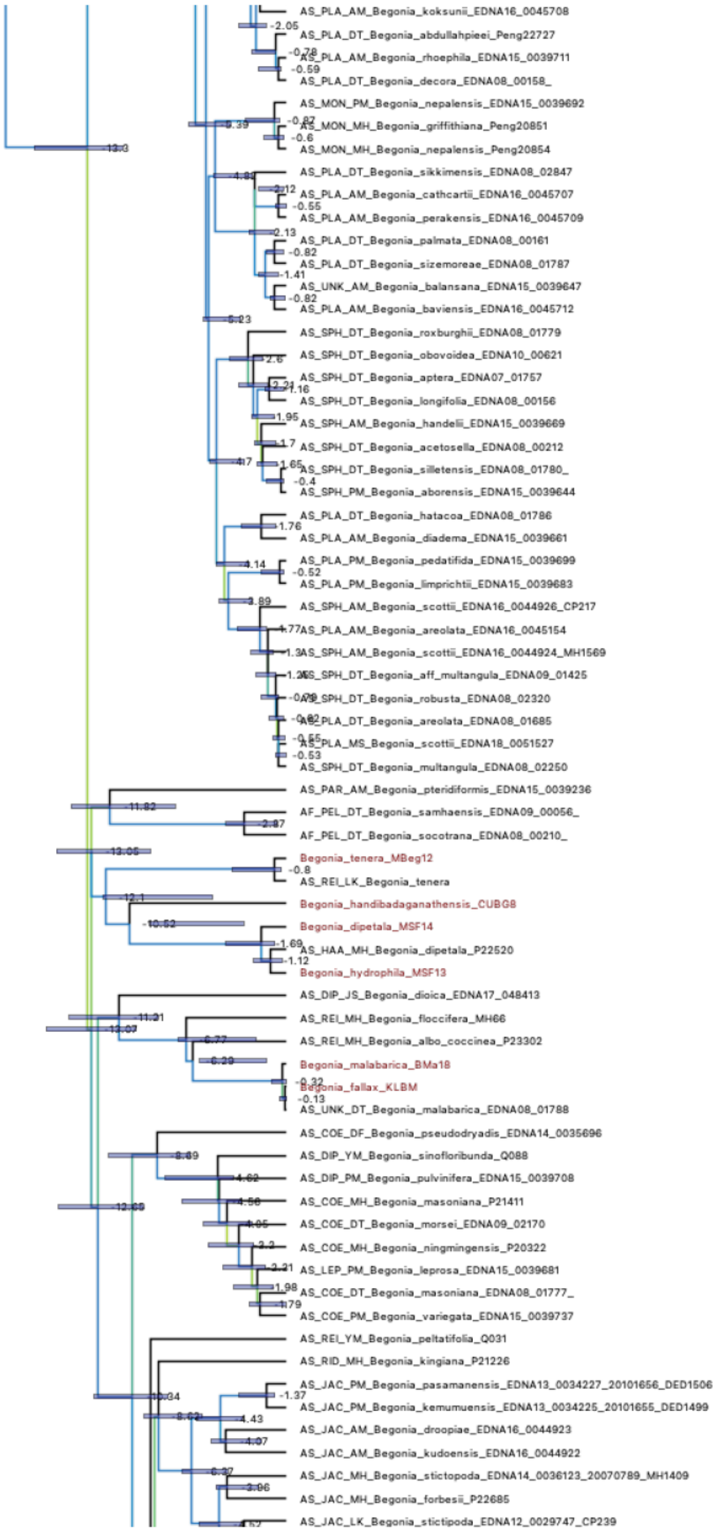
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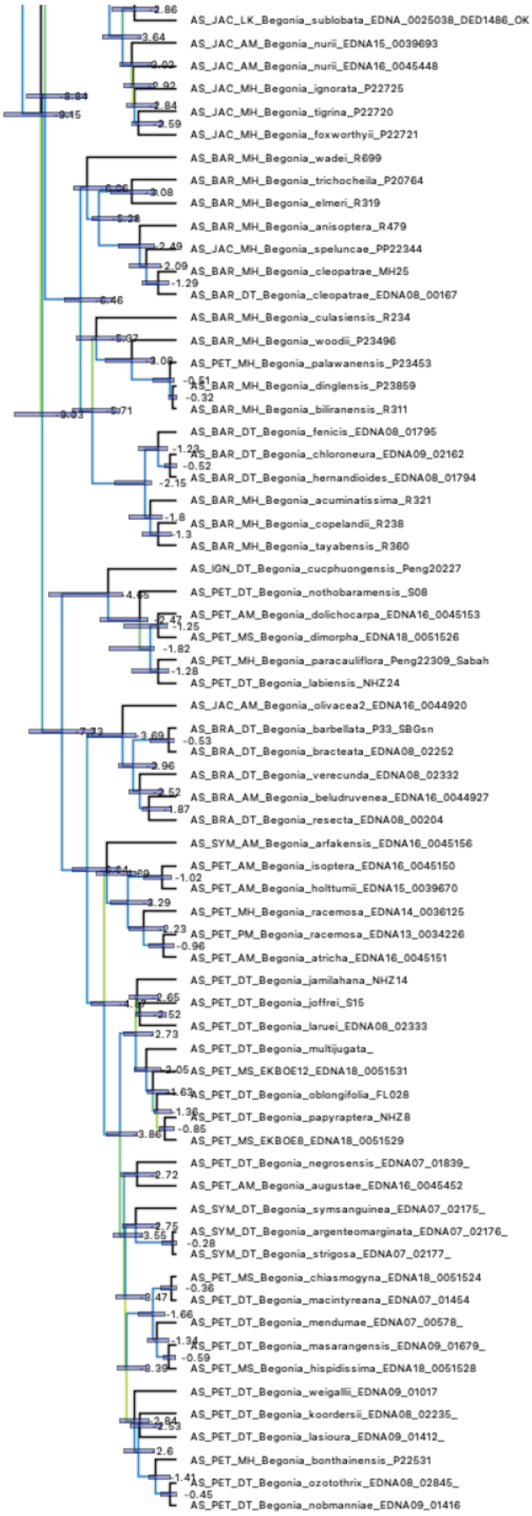
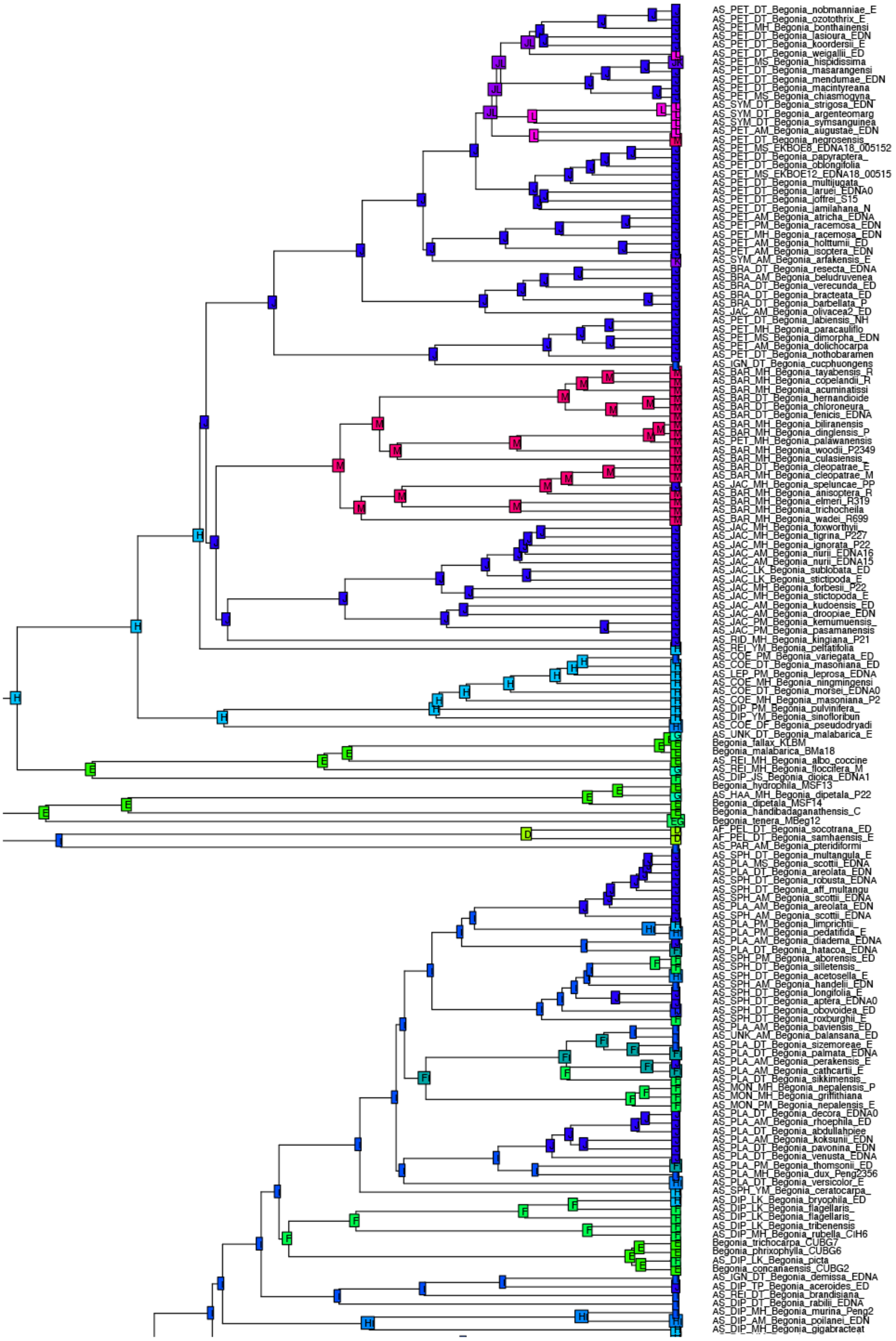


Figure 3.9: Time calibrated phylogeny of the family *Begoniaceae* for 371 taxa.

Samples in red show taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest. Collapsed branches are clades that hosted no taxa from the Western Ghats.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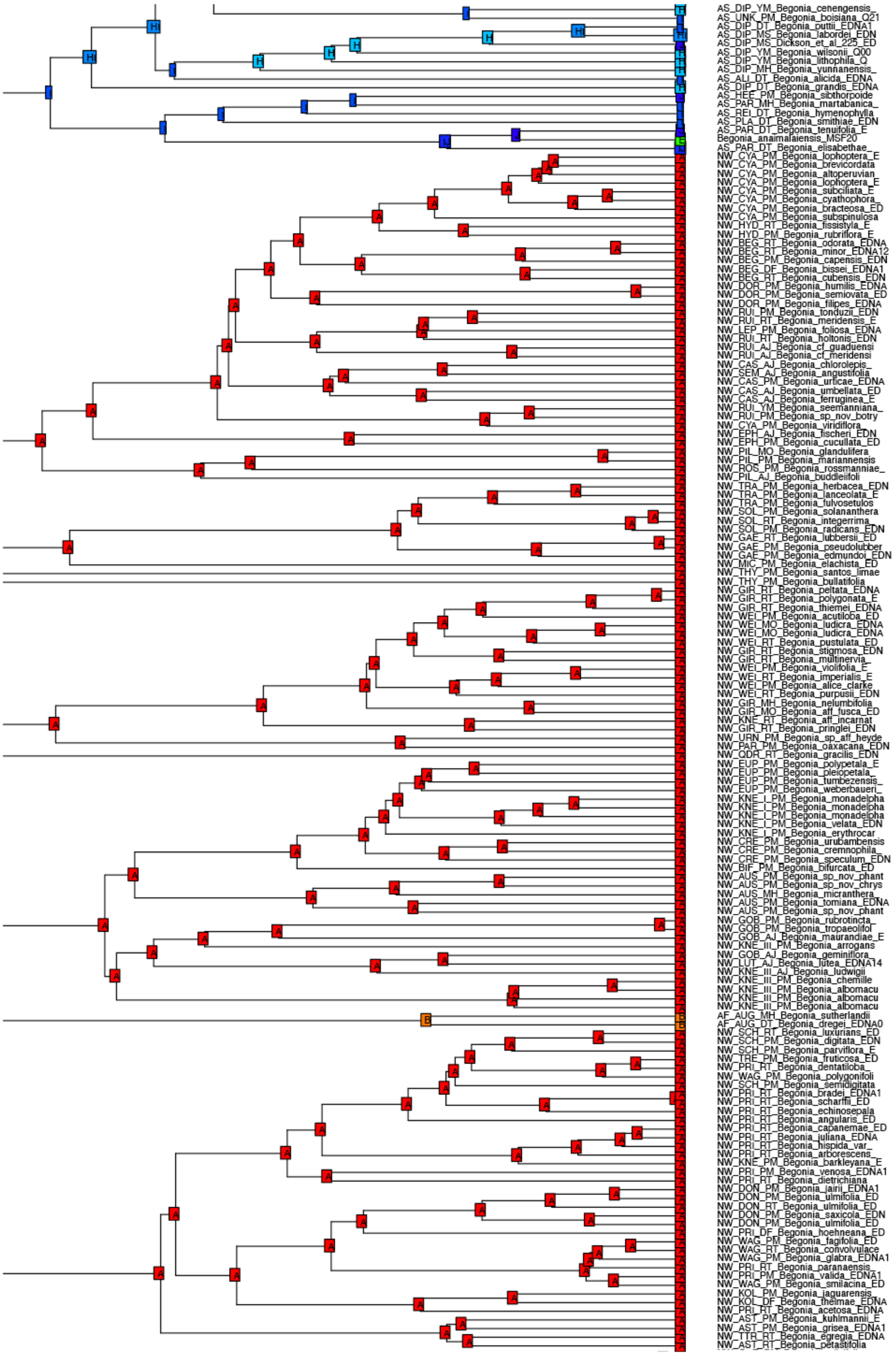
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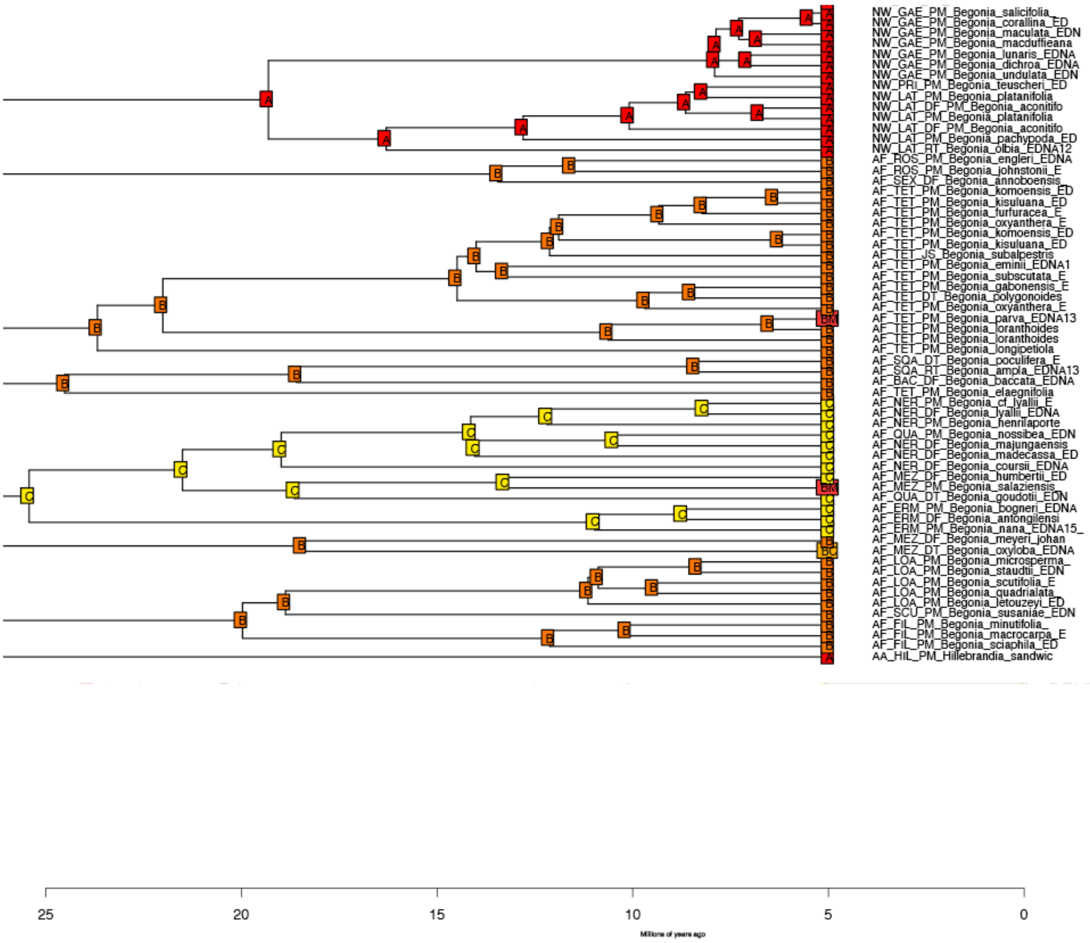


Figure 3.10: DEC+J ancestral area reconstruction for the family *Begoniaceae*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Socotra (Yellow green), E=Western Ghats (Light green), F=Himalayas (Neon green), G=Sri Lanka (Sea green), H=China (Light blue), I=Continental Asia (Indigo), J=Sunda Shelf (Royal blue), K=Sahul Shelf (Purple), L=PNG (Magenta), M=Philippines (Pink). LnL value of -388.44. Clades listed in Table 3.2.

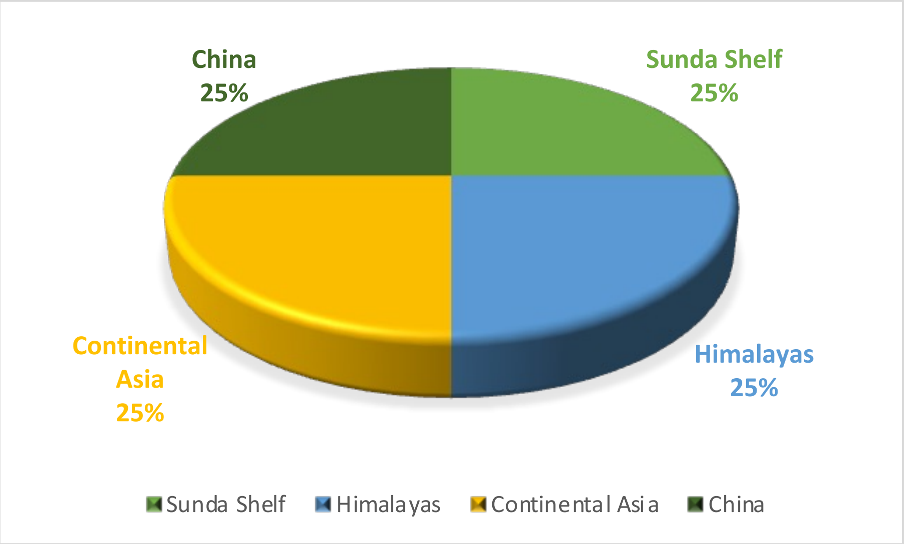


Figure 3.11: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Begoniaceae*.

Clade	**Taxa in clade**	**Minimum Age (mya)**	**Area Code**
Begoniaceae I	*Begonia anaimalaiensis MSF20*	3.13	J
Begoniaceae II	*Begonia trichocarpa CUBG7, Begonia phrixophylla CUBG6, Begonia concanensis CUBG2*	7.45	F
Begoniaceae III	*Begonia dipetala MSF14, Begonia hydrophila MSF13, Begonia tenera MBeg12, Begonia handibadaganathensis CUBG8*	13.05	I
Begoniaceae IV	*Begonia malabarica BMa18, Begonia fallax KLBM*	12.65	H

Table 3.2: *Begoniaceae* table showing the clade number, taxa found in each clade, their minimum age, and geographic origin.

3.3.3 *Chloranthaceae*

Maximum likelihood phylogenies were generated for the family *Chloranthaceae* using the target loci rbcL, rpl20, rps16, trnL, and ITS (Zhang et al., 2015). The ITS phylogeny (Figure 3.12) was better resolved than the chloroplast phylogeny. A dated phylogeny (Figure 3.13) was constructed for 44 taxa using the ITS alignment. A single clade was found endemic to the Western Ghats, it hosted the sample *Sarcandra grandifolia*, now *Sarcandra glabra subsp. brachstachys*. The species is widespread and is found in India, Sri Lanka, Continental Asia, and China. The clade was well supported and sat amongst taxa from Sri Lanka, China, Continental Asia, the Sunda Shelf, Papua New Guinea, and the Philippines. It had a minimum node age of 53.92 myr and showed a geographic origin signal from China, Continental Asia, and the Sunda and Sahul shelves (Figure 3.14). The family showed an overall age of 112 million years.

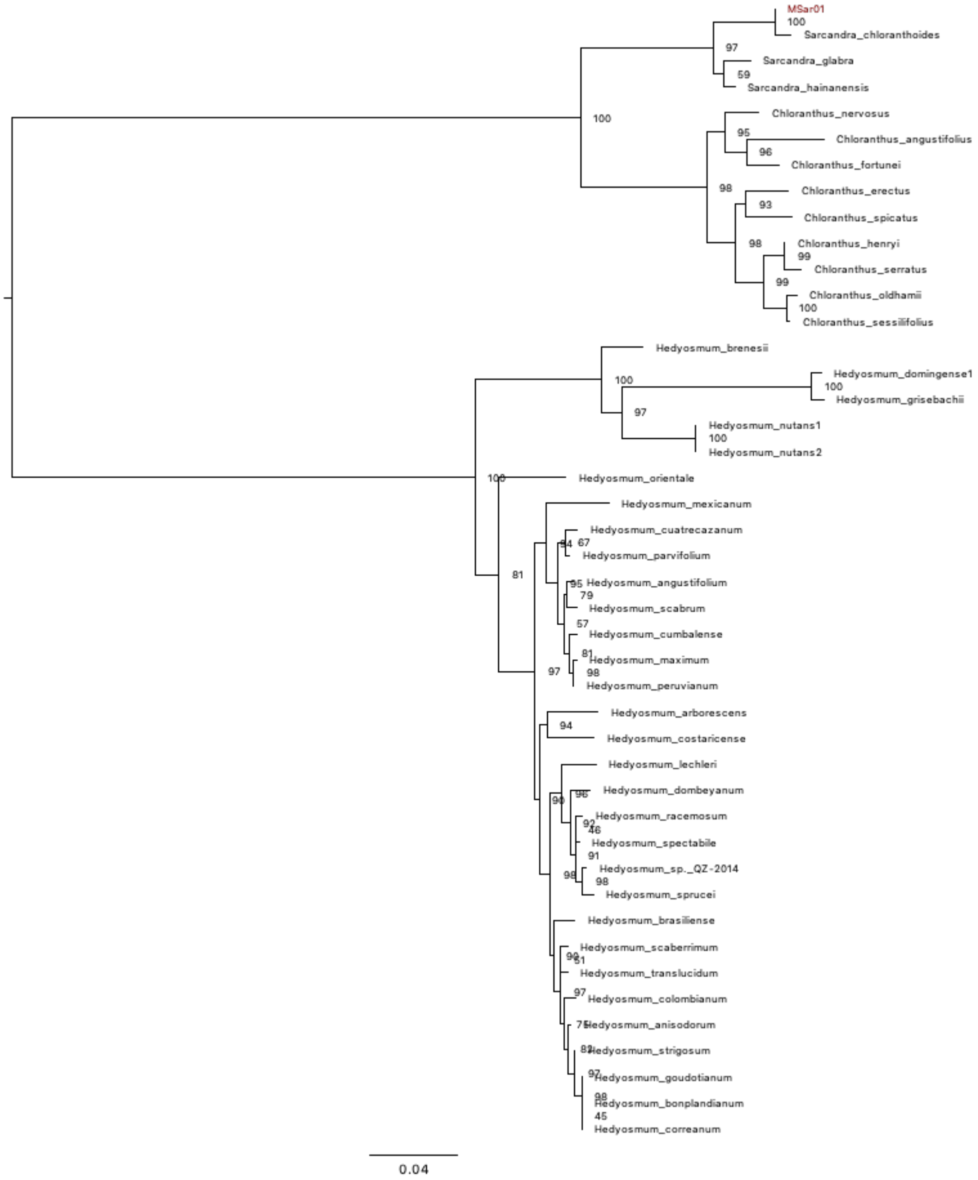


Figure 3.12: Maximum Likelihood phylogeny of the family *Chloranthaceae*.

The maximum likelihood phylogeny was generated for 44 taxa using IQTREE for ITS sequences. Sample in red indicates taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades.

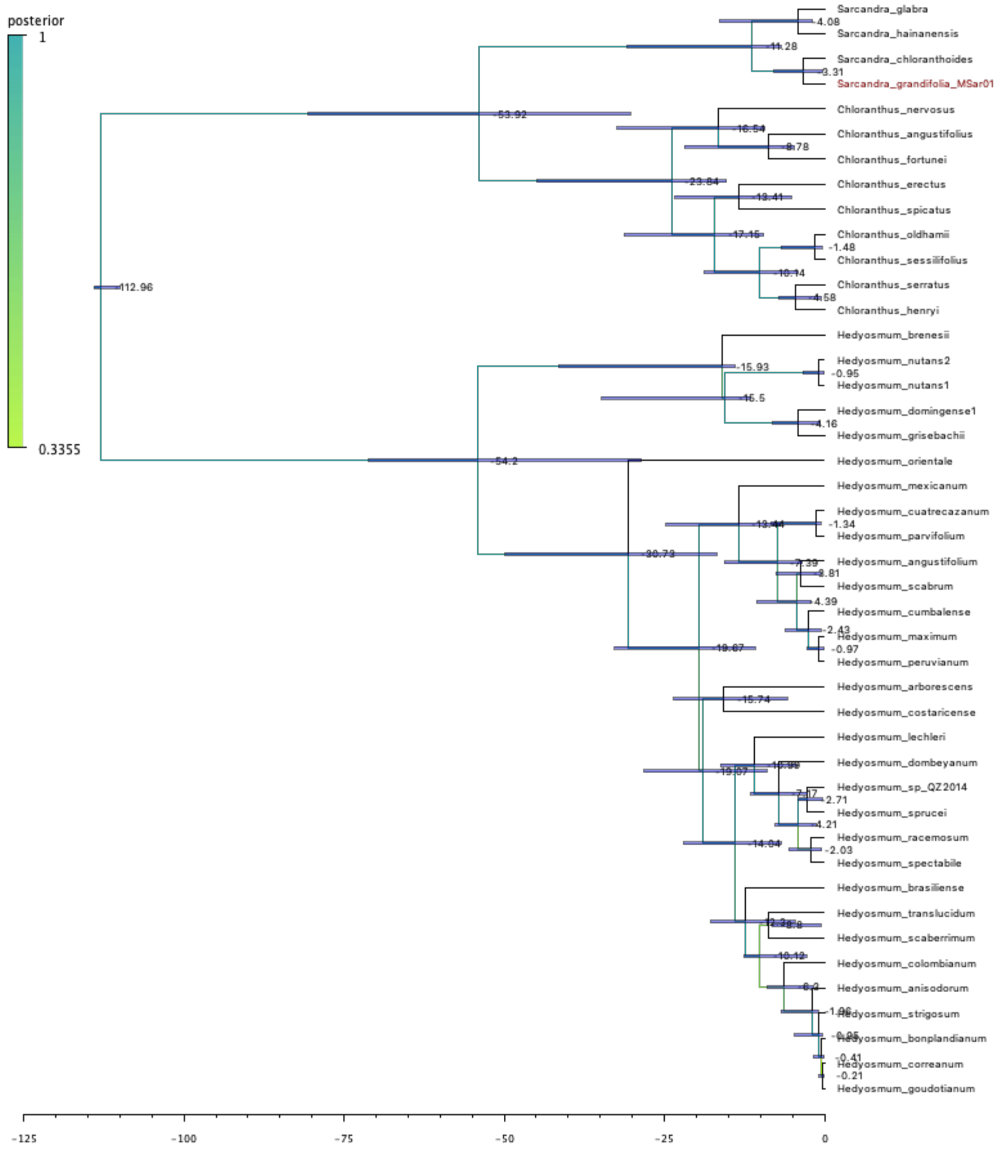


Figure 3.13: Time calibrated phylogeny of the family *Chloranthaceae* for 44 taxa.

Sample in red shows taxa native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest.

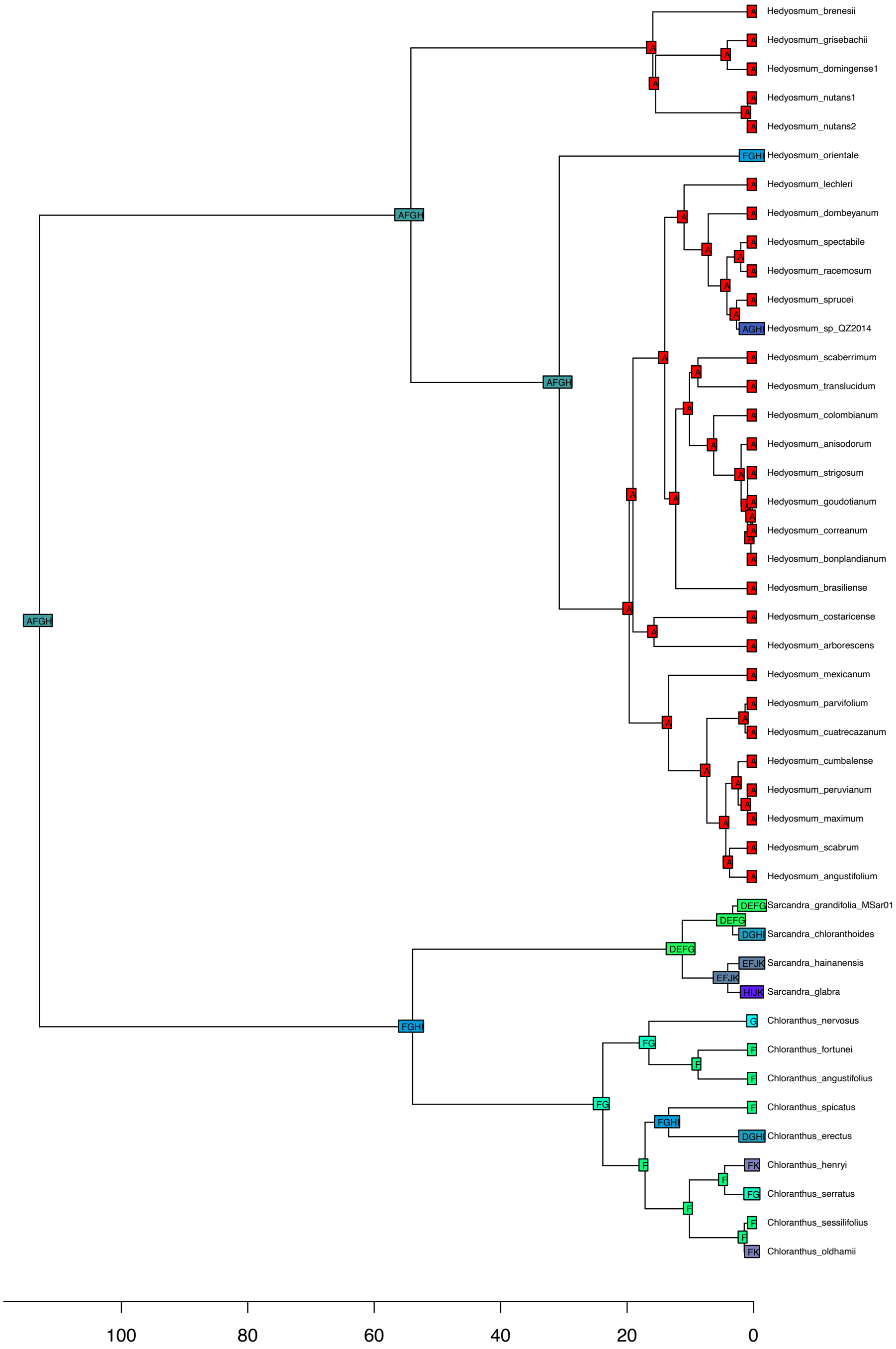


Figure 3.14: DEC+J ancestral area reconstruction for the family *Chloranthaceae*.

Geographic areas are coded as follows – A=America, D=India, E=Sri Lanka, F=China, G=Continental Asia, H=Sunda Shelf, I = Sahul Shelf, J=PNG, K=Philippines. LnL value -106.8

3.3.4 *Dipterocarpaceae*

Maximum likelihood (Figure 3.15) and time-calibrated (Figure 3.16) phylogenies were generated for a 158 taxa of the family *Dipterocarpaceae* using the target loci - matK, trnL, and trnF (Sanil et al., 2022). The dated phylogeny gave the family an age of c. 87.5 myr. Nine clades (Table 3.3) were found with taxa endemic or native to the Western Ghats. Maximum likelihood for the *Dipterocarpaceae*s found that individualspecies level clades were not well supported but the larger genus level clades were. Clade I included the taxa *Dipterocarpus bourdilonii* (PP 18), a Western Ghats endemic, found amongst taxa from Sri Lanka, Continental Asia, and the Sunda Shelf. Clade II was made of *Dipterocarpus indicus* (PP 12), a Western Ghats endemic, sister to samples from China, Continental Asia, and the Sunda Shelf. Clade III also included the taxa *Dipterocarpus bourdilonii* (PP 37), the clade sat amongst species from the Sunda Shelf, Continental Asia, and Sri Lanka. Although clade I and III had taxonomically identical species, the taxa placed very differently in the phylogenies. All three clades had a minimum node age of 14.96 myr and DEC+J analysis (Figure 3.17) indicated a Sunda Shelf origin.

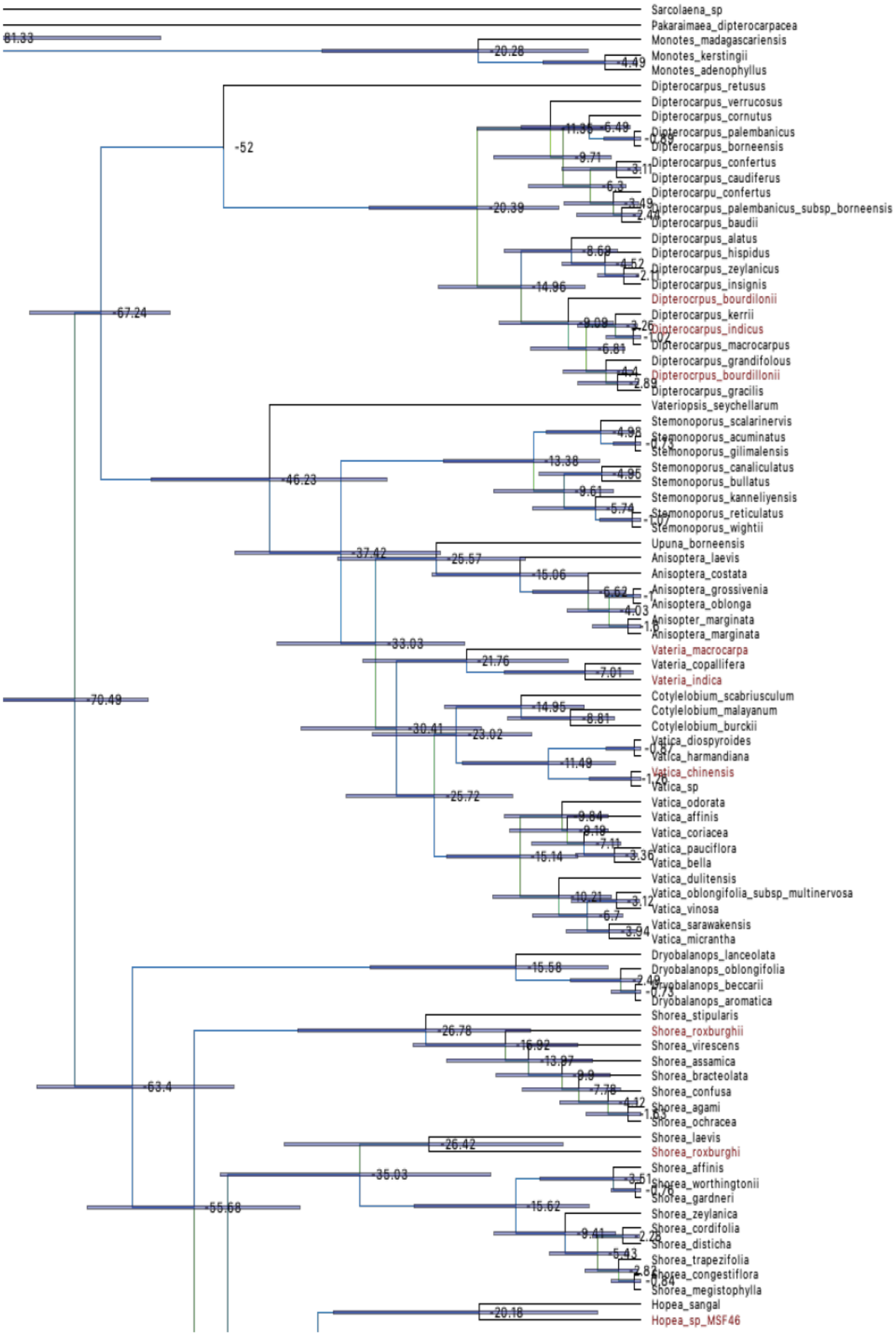
Clade IV hosted the taxa *Vateria macrocarpa* and *Vateria indica*, both Western Ghats endemics, clade was no well supported and sat amongst taxa from Sri Lanka. It had a minimum node age of 30.41 myr and showed signals form Sri Lanka and the Sunda Shelf. Clade V was the sample *Vatica chinensis*, a Ghats and Sri Lankan native found amongst taxa from Continental Asia and the Sunda Shelf. The clade had a minimum node age of 11.49 myr and indicated a Sunda Shelf origin. Clade VI (PP 46) and VII (PP 47) had the widespread taxa – *Shorea roxburghii*, now *Anthoshorea roxburghii.* The clades were taxonomically identical but placed very differently in the phylogenies. Clade VI had a minimum node age of 16.92 myr and Clade VII had a minimum node age of 26.42 myr. Both clades showed a Sunda Shelf signal of origin.

Clade VIII had the taxa *Hopea sp* (PP 82), a Western Ghats endemic present amongst samples from Sri Lanka, Continental Asia, and the Sunda Shelf. The clade had a minimum node age of 40.28 million years and showed Sunda Shelf origin. Clade IX had the taxa *Hopea canarensis*, *Hopea ponga* (PP 44), *Hopea racophloea* (PP 13), and *Hopea racholphea* (PP 35), *Hopea glabra* (PP 66), *Hopea erosa* (PP 62), *Hopea parviflora* (PP 62), *Hopea utilis* (PP 100/83), and *Hopea sasidharanii* (PP100/83) all endemic to the Western Ghats. *Hopea racophloea* and *Hopea racholphea* are taxonomically identical but placed differently in the phylogenies. The clade had a minimum node age of 32.17 million years and showed a Continental Asian and Sunda Shelf origin. Based on the time-calibrated phylogeny it appears that the family *Dipeterocarpaceae* first arrived to the Western Ghats 40.28 million years ago. The family has seen multiple dispersals to this tropical mountain range between c.7 and 40 million years ago. Dispersal to the Ghats has occurred predominantly from the Sunda Shelf.


Pakaraimaea_dipterocarpacea
Sarcolaena_sp
Monotes_madagascariensis
Monotes_adenophyllus
Monotes_kerstingii
Dipterocarpus_retusus
Dipterocarpus_baudii
Dipterocrpus_bourdilonii
Dipterocarpu_confertus
Dipterocarpus_borneensis
Dipterocarpus_palembanicus
Dipterocarpus_palembanicus_subsp_borneensis
Dipterocarpus_verrucosus
Dipterocarpus_caudiferus
Dipterocarpus_cornutus
Dipterocarpus_alatus
Dipterocarpus_hispidus
Dipterocarpus_insignis
Dipterocarpus_zeylanicus
Dipterocarpus_grandifolous
Dipterocarpus_gracilis
Dipterocarpus_kerrii
Dipterocarpus_confertus
Dipterocrpus_bourdillonii
Dipterocarpus_indicus
Dipterocarpus_macrocarpus
Vateriopsis_seychellarum
Stemonoporus_kanneliyensis
Stemonoporus_reticulatus
Stemonoporus_wightii
Stemonoporus_bullatus
Stemonoporus_canaliculatus
Stemonoporus_scalarinervis
Stemonoporus_acuminatus
Stemonoporus_gilimalensis
Upuna_borneensis
Anisoptera_laevis
Anisopter_marginata
Anisoptera_costata
Anisoptera_marginata
Anisoptera_grossivenia
Anisoptera_oblonga
Vateria_macrocarpa
Vateria_copallifera
Vateria_indica
Cotylelobium_scabriusculum
Cotylelobium_burckii
Cotylelobium_malayanum
Vatica_chinensis
Vatica_sp
Vatica_diospyroides
Vatica_harmandiana
Vatica_affinis
Vatica_odorata
Vatica_coriacea
Vatica_dulitensis
Vatica_oblongifolia_subsp_multinervosa
Vatica_vinosa
Vatica_bella
Vatica_pauciflora
Vatica_micrantha
Vatica_sarawakensis
Dryobalanops_lanceolata
Dryobalanops_aromatica
Dryobalanops_beccarii
Dryobalanops_oblongifolia
Shorea_stipularis
Shorea_virescens
Shorea_ochracea
Shorea_assamica
Shorea_agami
Shorea_roxburghii
Shorea_bracteolata
Shorea_confusa
Shorea_roxburghi
Shorea_laevis
Shorea_affinis
Shorea_gardneri
Shorea_worthingtonii
Shorea_zeylanica
Shorea_trapezifolia
Shorea_disticha
Shorea_megistophylla
Shorea_congestiflora
Shorea_cordifolia
Hopea_sp_MSF46
Hopea_sangal
Neobalanocarpus_heimii
Hopea_discolor
Hopea_jucunda
Hopea_helferi
Hopea_centipeda
Hopea_latifolia

Figure 3.15: Maximum Likelihood tree for the family *Dipterocarpaceae*.

The maximum likelihood phylogeny was generated for 158 taxa using IQTREE for the target loci matK, trnL, and trnF for 158 taxa. Samples in red indicate taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades.


Sarcolaena_sp
Pakaraimaea_dipterocarpacea
81.33
Monotes_madagascariensis
20.28
Monotes_kerstingii
4.49
Monotes_adenophyllus
Dipterocarpus_retusus
Dipterocarpus_verrucosus
Dipterocarpus_cornutus
11.86
6.49
Dipterocarpus_palembanicus
0.89
Dipterocarpus_borneensis
52
9.71
Dipterocarpus_confertus
3.11
Dipterocarpus_caudiferus
6.3
Dipterocarpu_confertus
3.49
Dipterocarpus_palembanicus_subsp_borneensis
2.44
20.39
Dipterocarpus_baudii
Dipterocarpus_alatus
8.68
Dipterocarpus_hispidus
4.52
Dipterocarpus_zeylanicus
2.1
Dipterocarpus_insignis
14.96
Dipterocrpus_bourdilonii
67.24
Dipterocarpus_kerrii
9.08
3.26
Dipterocarpus_indicus
1.02
Dipterocarpus_macrocarpus
6.81
Dipterocarpus_grandifolous
4.4
Dipterocrpus_bourdillonii
2.89
Dipterocarpus_gracilis
Vateriopsis_seychellarum
Stemonoporus_scalarinervis
4.98
Stemonoporus_acuminatus
0.73
Stemonoporus_gilimalensis
13.38
Stemonoporus_canaliculatus
46.23
4.96
Stemonoporus_bullatus
9.61
Stemonoporus_kanneliyensis
5.74
Stemonoporus_reticulatus
1.07
Stemonoporus_wightii
Upuna_borneensis
37.42
Anisoptera_laevis
26.57
Anisoptera_costata
15.06
6.62
Anisoptera_grossivenia
1
Anisoptera_oblonga
4.03
Anisopter_marginata
1.8
Anisoptera_marginata
33.03
Vateria_macrocarpa
21.76
Vateria_copallifera
7.01
Vateria_indica
Cotylelobium_scabriusculum
70.49
14.95
Cotylelobium_malayanum
8.81
Cotylelobium_burckii
30.41
23.02
Vatica_diospyroides
0.87
Vatica_harmandiana
11.49
Vatica_chinensis
1.26
Vatica_sp
25.72
Vatica_odorata
9.84
Vatica_affinis
9.19
Vatica_coriacea
7.11
Vatica_pauciflora
15.14
3.36
Vatica_bella
Vatica_dulitensis
Vatica_oblongifolia_subsp_multinervosa
10.21
3.12
Vatica_vinosa
6.7
Vatica_sarawakensis
3.94
Vatica_micrantha
Dryobalanops_lanceolata
15.58
Dryobalanops_oblongifolia
2.49
Dryobalanops_beccarii
0.73
Dryobalanops_aromatica
Shorea_stipularis
26.78
Shorea_roxburghii
16.92
Shorea_virescens
13.97
Shorea_assamica
9.9
Shorea_bracteolata
63.4
7.78
Shorea_confusa
4.12
Shorea_agami
1.63
Shorea_ochracea
Shorea_laevis
26.42
Shorea_roxburghi
Shorea_affinis
35.03
3.51
Shorea_worthingtonii
0.76
Shorea_gardneri
15.62
55.68
Shorea_zeylanica
Shorea_cordifolia
9.41
2.28
Shorea_disticha
5.43
Shorea_trapezifolia
2.87
Shorea_congestiflora
0.84
Shorea_megistophylla
Hopea_sangal
20.18
Hopea_sp_MSF46

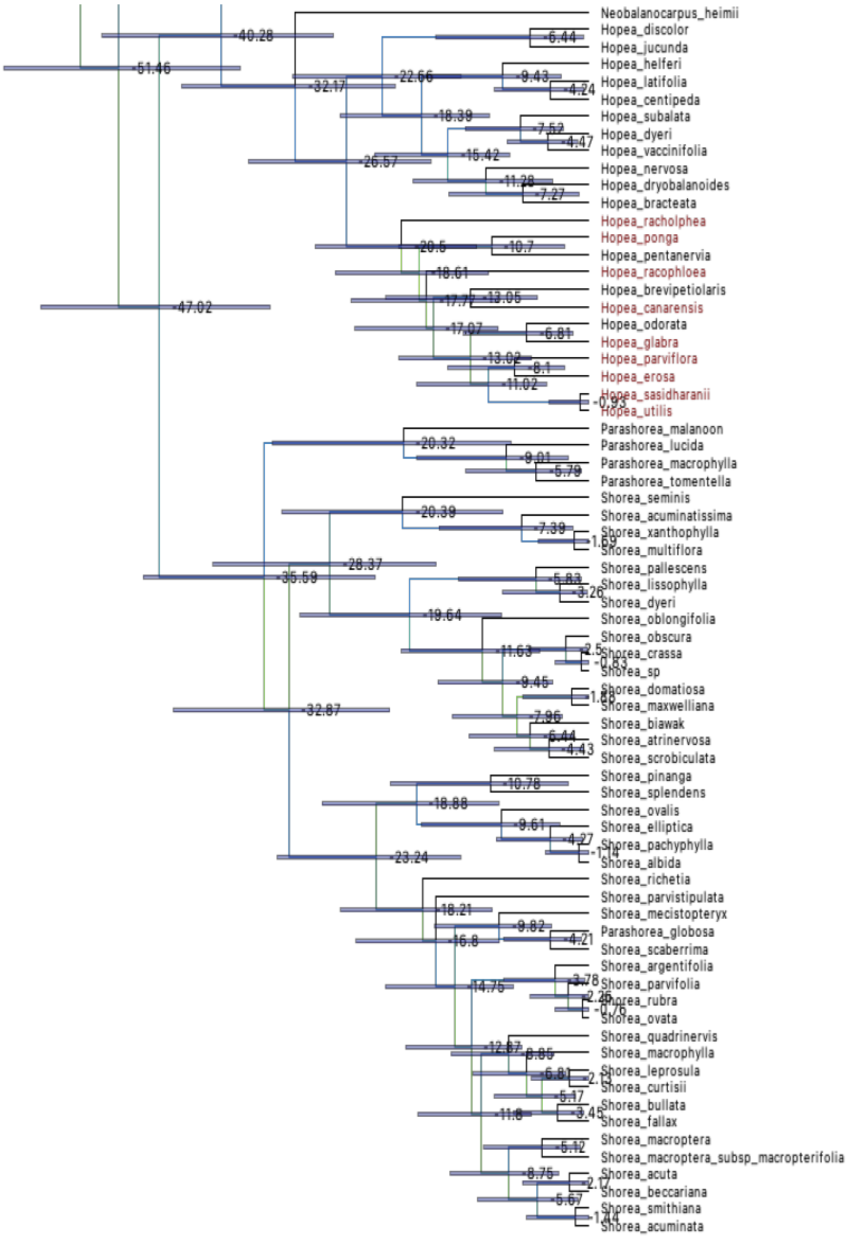
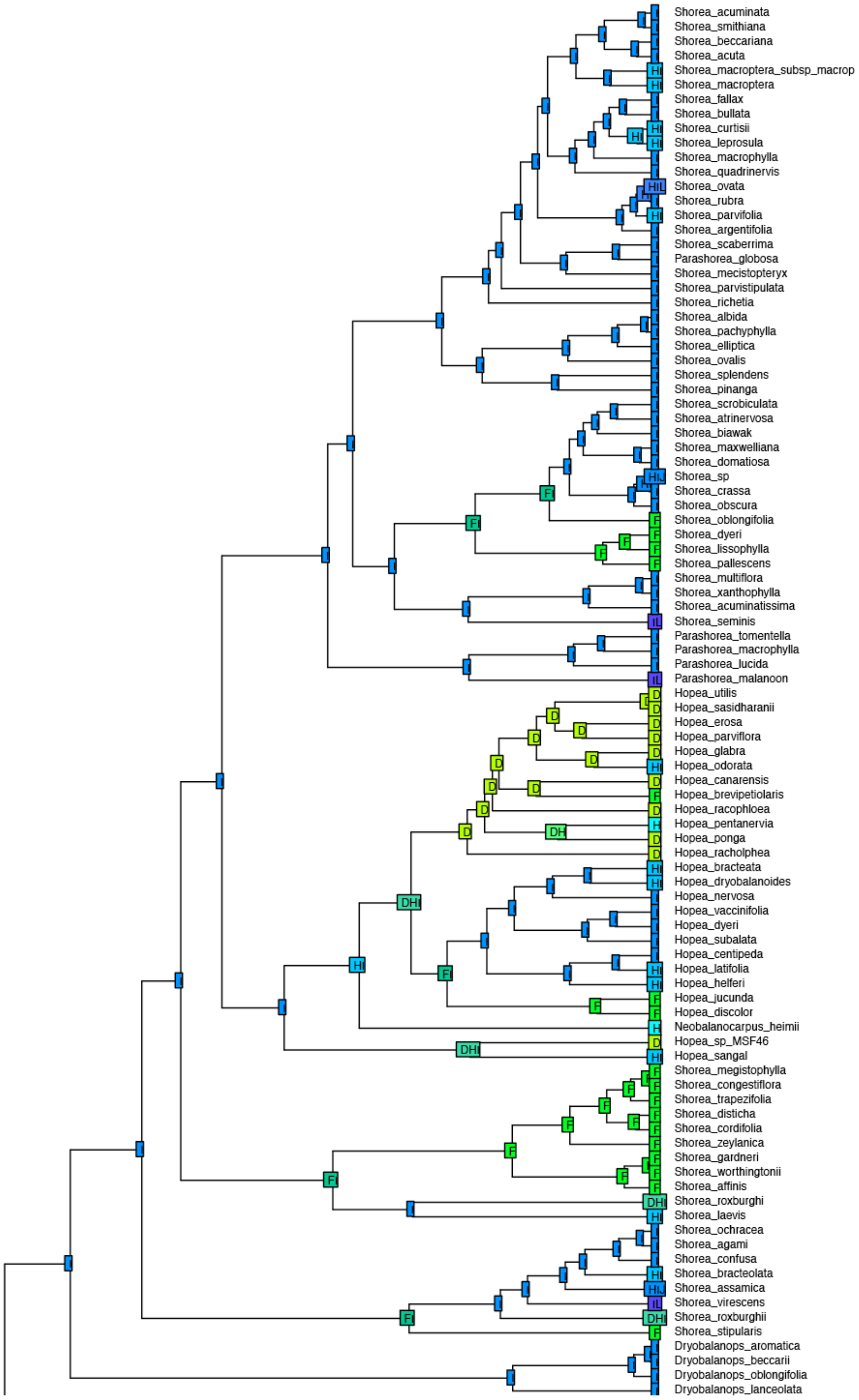


Figure 3.16: Time calibrated phylogeny of the family *Dipterocarpaceae* for 158 taxa.

Samples in red depict taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest.


Shorea_acuminata
Shorea_smithiana
Shorea_beccariana
Shorea_acuta
Shorea_macroptera_subsp_macrop
Shorea_macroptera
Shorea_fallax
Shorea_bullata
Shorea_curtisii
Shorea_leprosula
Shorea_macrophylla
Shorea_quadrinervis
Shorea_ovata
Shorea_rubra
Shorea_parvifolia
Shorea_argentifolia
Shorea_scaberrima
Parashorea_globosa
Shorea_mecistopteryx
Shorea_parvistipulata
Shorea_richetia
Shorea_albida
Shorea_pachyphylla
Shorea_elliptica
Shorea_ovalis
Shorea_splendens
Shorea_pinanga
Shorea_scrobiculata
Shorea_atrinervosa
Shorea_biawak
Shorea_maxwelliana
Shorea_domatiosa
Shorea_sp
Shorea_crassa
Shorea_obscura
Shorea_oblongifolia
Shorea_dyeri
Shorea_lissophylla
Shorea_pallescens
Shorea_multiflora
Shorea_xanthophylla
Shorea_acuminatissima
Shorea_seminis
Parashorea_tomentella
Parashorea_macrophylla
Parashorea_lucida
Parashorea_malanoon
Hopea_utilis
Hopea_sasidharanii
Hopea_erosa
Hopea_parviflora
Hopea_glabra
Hopea_odorata
Hopea_canarensis
Hopea_brevipetiolaris
Hopea_racophloea
Hopea_pentanervia
Hopea_ponga
Hopea_racholphea
Hopea_bracteata
Hopea_dryobalanoides
Hopea_nervosa
Hopea_vaccinifolia
Hopea_dyeri
Hopea_subalata
Hopea_centipeda
Hopea_latifolia
Hopea_helferi
Hopea_jucunda
Hopea_discolor
Neobalanocarpus_heimii
Hopea_sp_MSF46
Hopea_sangal
Shorea_megistophylla
Shorea_congestiflora
Shorea_trapezifolia
Shorea_disticha
Shorea_cordifolia
Shorea_zeylanica
Shorea_gardneri
Shorea_worthingtonii
Shorea_affinis
Shorea_roxburghi
Shorea_laevis
Shorea_ochracea
Shorea_agami
Shorea_confusa
Shorea_bracteolata
Shorea_assamica
Shorea_virescens
Shorea_roxburghii
Shorea_stipularis
Dryobalanops_aromatica
Dryobalanops_beccarii
Dryobalanops_oblongifolia
Dryobalanops_lanceolata

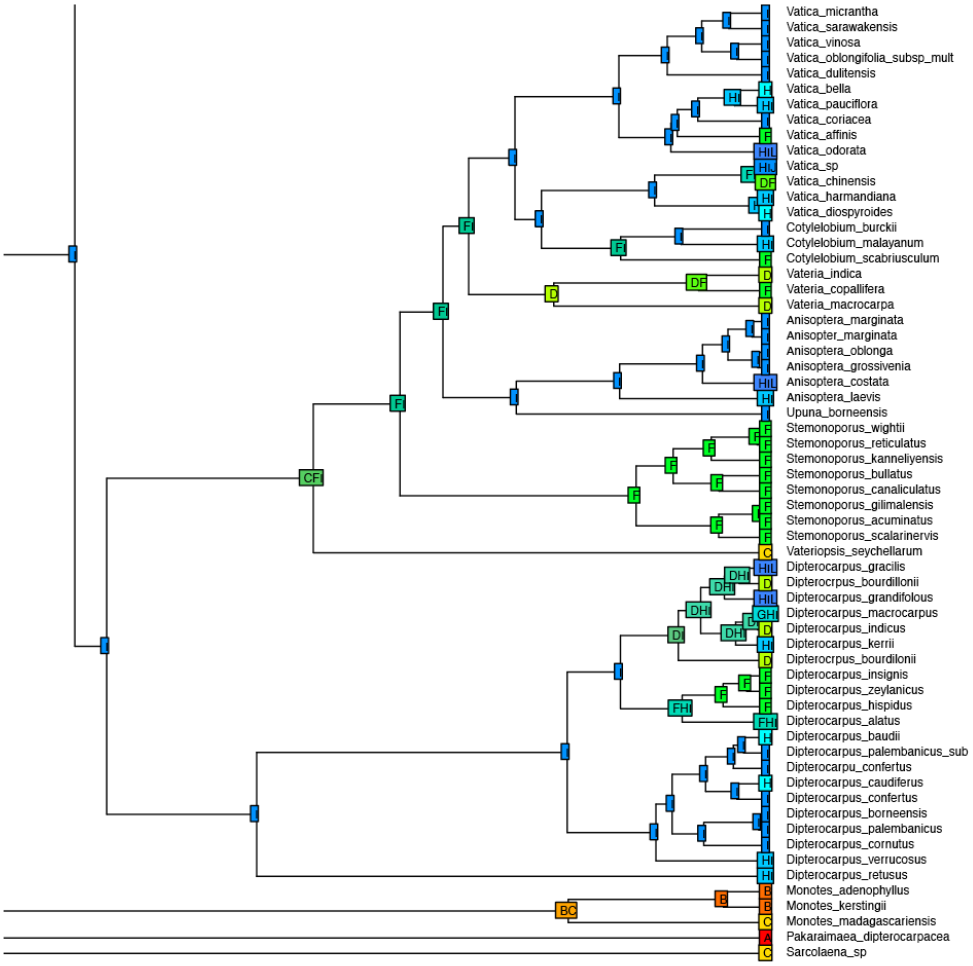


Figure 3.17: DEC+J ancestral area reconstruction for the family *Dipterocarpaceae*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Western Ghats (Light green), F=Sri Lanka (Neon green), H=Continental Asia (Light blue), I=Sunda Shelf (Indigo). LnL value of -390.08. Clades listed in Table 3.3.

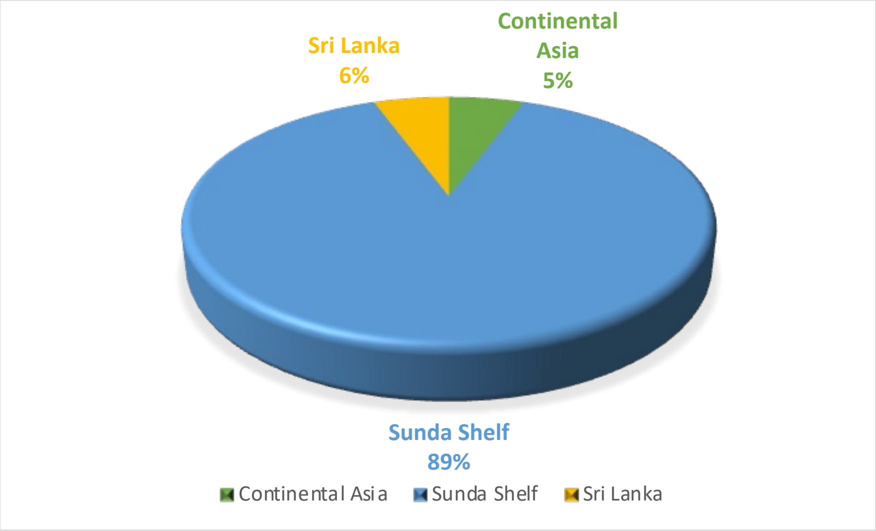


Figure 3.18: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Dipterocarpaceae*.

Clade	**Taxa in the clade**	**Minimum age (mya)**	**Area Code**
Dipterocarpaceae I	*Dipterocrpus bourdilonii*	14.96	I
Dipterocarpaceae II	*Dipterocarpus indicus*	14.96	I
Dipterocarpaceae III	*Dipterocrpus bourdilonii*	14.96	I
Dipterocarpaceae IV	*Vateria macrocarpa, Vateria indica*	30.41	FI
Dipterocarpaceae V	*Vatica chinensis*	11.49	I
Dipterocarpaceae VI	*Shorea roxburghii*	16.92	I
Dipterocarpaceae VII	*Shorea roxburghi*	26.42	I
Dipterocarpaceae VIII	*Hopea sp MSF46*	40.28	I
Dipterocarpaceae IX	*Hopea canarensis, Hopea ponga, Hopea racophloea, Hopea racholphea, Hopea glabra, Hopea erosa, Hopea parviflora, Hopea utilis, Hopea sasidharanii*	32.17	HI

Table 3.3: *Dipterocarpaceae* table showing clade number, taxa found in each clade, their minimum age, and geographic origin.

3.3.5 *Ebenaceae*

Maximum likelihood (Figure 3.19) and time-calibrated (Figure 3.20) phylogenies were generated for 228 taxa of the family *Ebenaceae* focused on the genus *Diospyros* using the target loci atpB, rbcL, matK, and trnS (Turner et al., 2013). The dated phylogeny indicated that the genus *Diospyros* split away from *Ebenaceae* approximately 95 million years ago. Eight clades (Table 3.4) were found with taxa endemic or native to the Western Ghats, these are highlighted red in these phylogenies. The phylogeny was relatively well supported for most clades unless otherwise specified. Clade I hosted the widespread and taxonomic nightmare *Diospyros ferrea* (PP 87), it was placed amongst other *Diospyros ferrea* from around the world. The clade had a minimum node age 13.14 myr and showed Continental Asian origin. Clade II included the Western Ghats endemic *Diospyros bourdilonii* (PP 90), it placed amongst taxa from Continental Asia. The clade had a minimum node age of 42.87 myr and showed a Continental Asian signal.

Clade III had the taxa *Diospyros melanoxylon* and *Diospyros affinis* (PP 97/10), both Western Ghats and Sri Lankan natives found amongst samples from Continental Asia, and the Sunda and Sahul shelves. The clade had a minimum node age of 29.04 myr and indicated a Sunda Shelf origin. Clade IV was made of the Western Ghats and Sunda Shelf native, *Diospyros ridleyi* (PP 100/84), the clade sat between taxa from America, Continental Asia, and the Sunda Shelf. It had a minimum node age of 8.44 myr and showed roots in Continental Asia and the Sunda Shelf. Clade V was well supported and had the taxa *Diospyros malabarica1* and *Diospyros malabarica_MDio09*, the taxa are taxonomically identical but place sister in the phylogenies. The clade had a minimum node age of 28.47 myr and originated from Continental Asia. Clade VI was well supported and had the taxa *Diospyros pruriens*, a Western Ghats endemic, sat amongst taxa from Continental Asia and the Sunda Shelf. It had a minimum node age of 20.86 myr and showed a Continental Asian origin.

Clade VII had the taxa *Diospyros ebenum* and *Diospyros montana*, the clade was well supported and sat sister to taxa from Sri Lanka and Continental Asia. *Diospyros ebenum* is native to the Western Ghats and Sri Lanka, while *Diospyros montana* is a widespread species found throughout tropical Asia. The clade had a minimum node age of 25.22 myr and showed a Continental Asian signal of origin. Clade VIII hosted the taxa *Diospyros sylvatica* a native of the Western Ghats and Sri Lanka. The clade is well supported and was amongst taxa from Continental Asia and the Sunda Shelf. The dated phylogeny showed that the genus *Diospyros* arrived several times to the Western Ghats between c.8 and 42 million years ago. DEC+J analysis (Figure 3.21) showed this genus to have arrived to the Western Ghats largely from Continental Asia and partially the Sunda Shelf.


Lissocarpa_guianensis
100
Lissocarpa_benthamii
100
Lissocarpa_kating
100
Royena_glabra
92
Royena_zombensis
100
Royena_lucida1
100
Royena_cordata
96
Royena_sp
99
Royena_lycioides
78
Royena_whyteana
100
Euclea_pseudebenus
Euclea_sp1
100
52
Euclea_crispa1
57
Euclea_divinorum
95
Euclea_natalensis
55
Euclea_undulata
47
Euclea_racemosa
Euclea_sp2
Diospyros_maingayi
100
Diospyros_puncticulosa
Diospyros_pentamera
100
Diospyros_australis_NM
100
Diospyros_macrocarpa2
100
Diospyros_oubatchensis1
54
Diospyros_margaretae
91
Diospyros_balansae
87
Diospyros_brassica
Diospyros_eriantha
Diospyros_fragrans
100
Diospyros_mannii
69
Diospyros_artanthifolia
90
Diospyros_dichroa
79
Diospyros_vestita
78
Diospyros_carbonaria
67
34
75
Diospyros_ropourea
Diospyros_tricolor_NM
100
Diospyros_iturensis
99
Diospyros_cooperi
11
10
Diospyros_batocana1
100
36
Diospyros_melocarpa
14
Diospyros_bipindensis
45
Diospyros_obliquifolia
Diospyros_dendo
100
Diospyros_gilletii
Diospyros_gabunensis
92
Diospyros_scabra
35
Diospyros_dicorypheoides
96
Diospyros_cinnamomoides
100
27
Diospyros_parvifolia
Diospyros_cf_clusiifolia
80
Tetraclis_baronii
68
99
Diospyros_fuscovelutina
86
Diospyros_vescoi
Diospyros_aculeata
Diospyros_boivinii
92
Diospyros_erythrosperma
100
13
43
Diospyros_velutipes
79
Diospyros_anosivolensis
100
Diospyros_gracilipes1
98
37
Diospyros_leucocalyx
29
Diospyros_natalensis
100
Diospyros_olacinoides
73
Diospyros_comorensis
100
Diospyros_squamosa
100
Diospyros_pruinosa
99
Diospyros_stenocarpa
Diospyros_ebenifera
100
Diospyros_tampinensis
99
100
Diospyros_microrhombus
100
Diospyros_rubripetiolata
100
Diospyros_mangabensis
100
Diospyros_sphaerosepala
Diospyros_lokohensis
87
Diospyros_occlusa
100
Maba_magnifolia
100
Diospyros_perrieri
100
Diospyros_tesselaria1
85
71
Diospyros_analamerensis1
63
Diospyros_consolatae
46
Diospyros_cupulifera
99
Diospyros_diversifolia1
Diospyros_borbonica
61
Diospyros_nodosa1
47
100
Diospyros_pterocalyx1
89
Diospyros_chrysophyllos1
Diospyros_neraudii1
98
98
44
Diospyros_revaughanii1
73
Diospyros_egrettarum1
83
Diospyros_hemiteles1
99
65
Diospyros_leucomelas1
76
Diospyros_boutoniana1
97
Diospyros_melanida1
Diospyros_humbertiana
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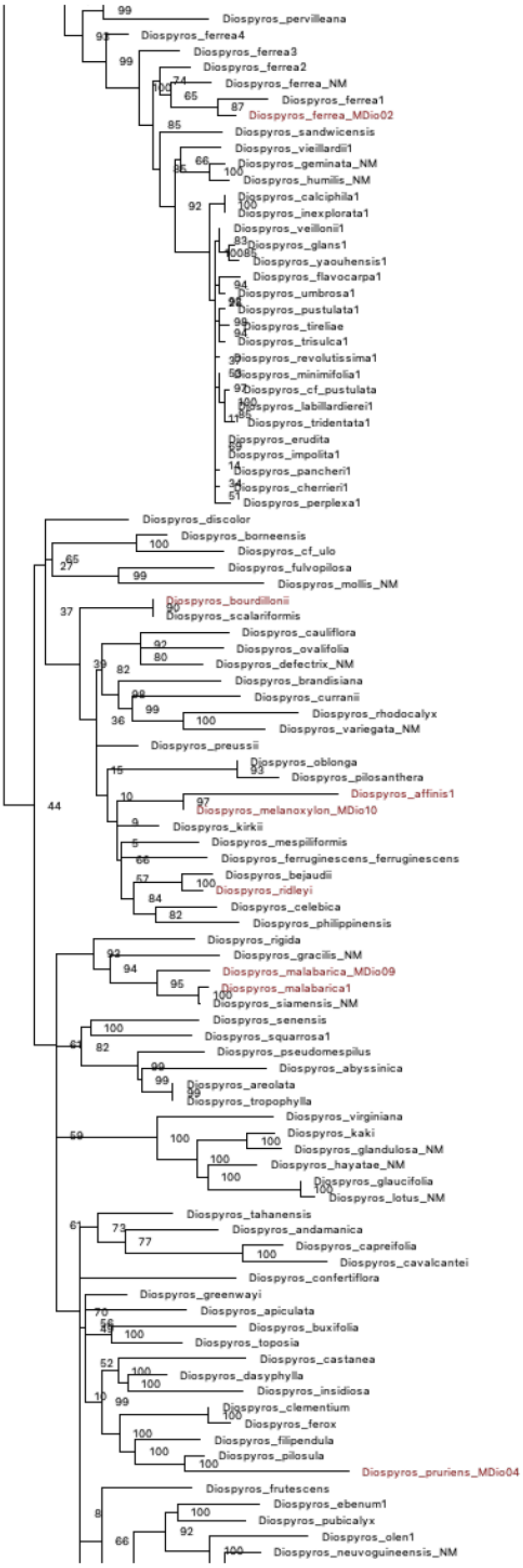
Diospyros_myriophylla
99
Diospyros_myrtifolia
48
Diospyros_haplostylis


Diospyros_pervilleana
Diospyros_ferrea4
Diospyros_ferrea3
Diospyros_ferrea2
Diospyros_ferrea_NM
Diospyros_ferrea1
Diospyros_ferrea_MDio02
Diospyros_sandwicensis
Diospyros_vieillardii1
Diospyros_geminata_NM
Diospyros_humilis_NM
Diospyros_calciphila1
Diospyros_inexplorata1
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Diospyros_glans1
Diospyros_yaouhensis1
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Diospyros_umbrosa1
Diospyros_pustulata1
Diospyros_tireliae
Diospyros_trisulca1
Diospyros_revolutissima1
Diospyros_minimifolia1
Diospyros_cf_pustulata
Diospyros_labillardierei1
Diospyros_tridentata1
Diospyros_erudita
Diospyros_impolita1
Diospyros_pancheri1
Diospyros_cherrieri1
Diospyros_perplexa1
Diospyros_discolor
Diospyros_borneensis
Diospyros_cf_ulo
Diospyros_fulvopilosa
Diospyros_mollis_NM
Diospyros_bourdillonii
Diospyros_scalariformis
Diospyros_cauliflora
Diospyros_ovalifolia
Diospyros_defectrix_NM
Diospyros_brandisiana
Diospyros_curranii
Diospyros_rhodocalyx
Diospyros_variegata_NM
Diospyros_preussii
Diospyros_oblonga
Diospyros_pilosanthera
Diospyros_affinis1
Diospyros_melanoxylon_MDio10
Diospyros_kirkii
Diospyros_mespiliformis
Diospyros_ferruginescens_ferruginescens
Diospyros_bejaudii
Diospyros_ridleyi
Diospyros_celebica
Diospyros_philippinensis
Diospyros_rigida
Diospyros_gracilis_NM
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Diospyros_siamensis_NM
Diospyros_senensis
Diospyros_squarrosa1
Diospyros_pseudomespilus
Diospyros_abyssinica
Diospyros_areolata
Diospyros_tropophylla
Diospyros_virginiana
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Diospyros_glandulosa_NM
Diospyros_hayatae_NM
Diospyros_glaucifolia
Diospyros_lotus_NM
Diospyros_tahanensis
Diospyros_andamanica
Diospyros_capreifolia
Diospyros_cavalcantei
Diospyros_confertiflora
Diospyros_greenwayi
Diospyros_apiculata
Diospyros_buxifolia
Diospyros_toposia
Diospyros_castanea
Diospyros_dasyphylla
Diospyros_insidiosa
Diospyros_clementium
Diospyros_ferox
Diospyros_filipendula
Diospyros_pilosula
Diospyros_pruriens_MDio04
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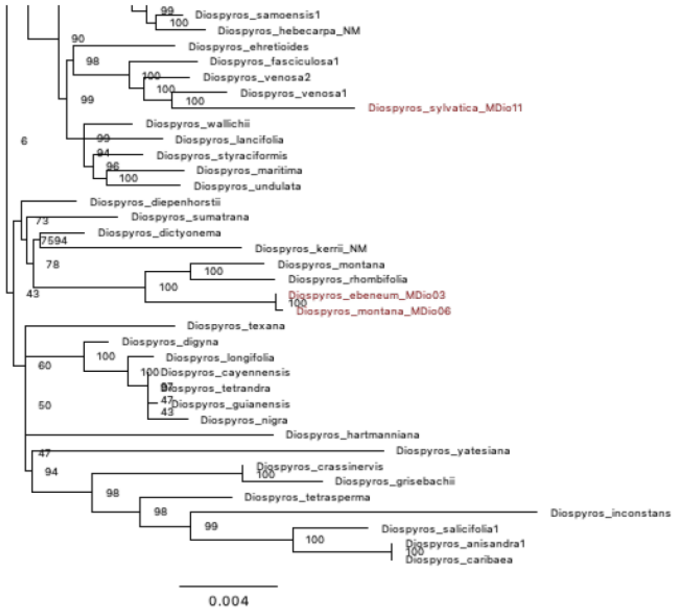
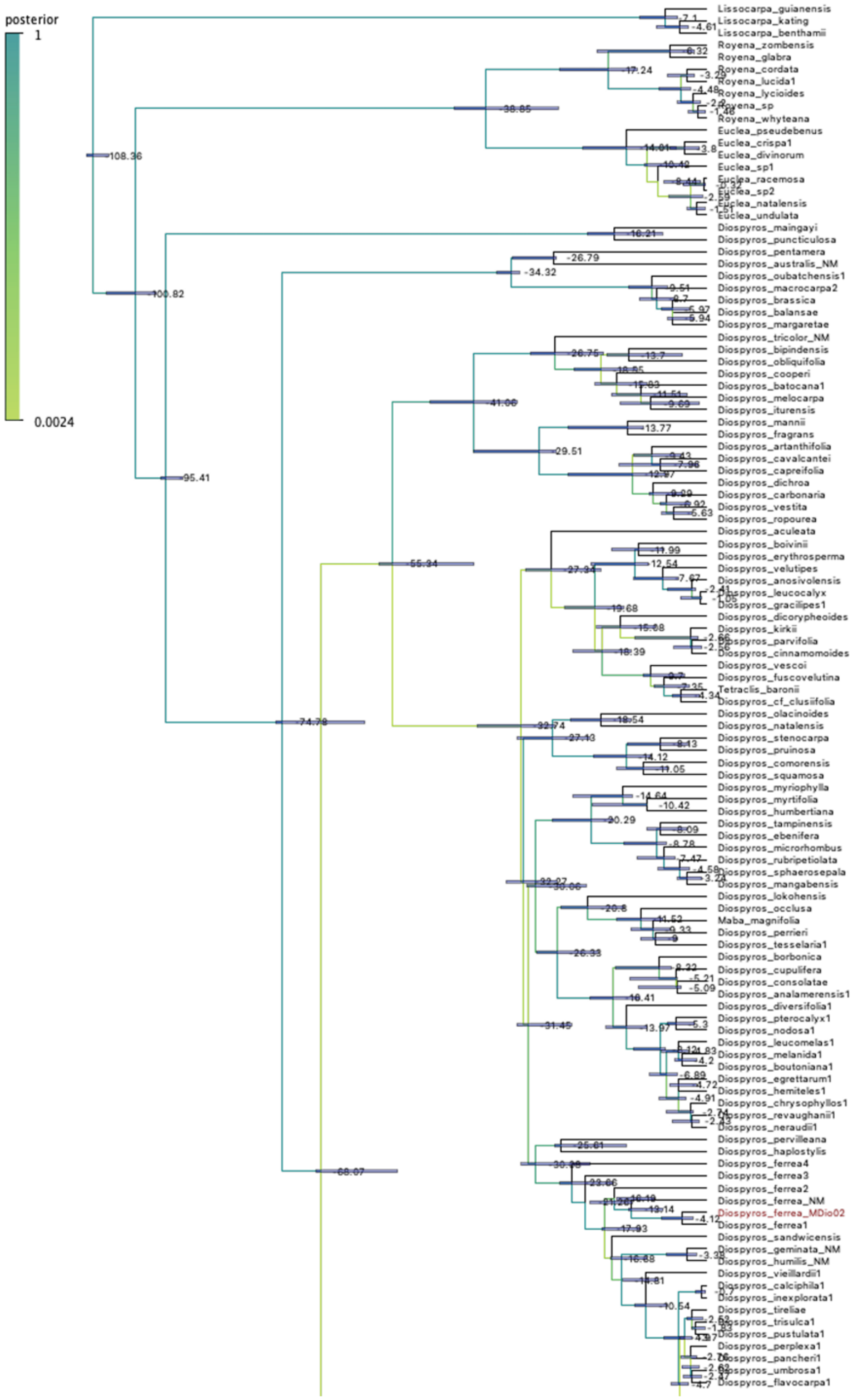


Figure 3.19: Maximum Likelihood phylogeny for the family *Ebenaceae* focused on genus *Diospyros*.

The maximum likelihood phylogeny was generated for 228 taxa using IQTREE for the target loci atpB, rbcL, matK, and trnS. Samples in red indicate taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades.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100.82
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74.78
68.07
55.34
38.85
17.24
14.01
10.42
34.32
26.79
41.08
26.75
29.51
13.77
12.07
27.34
19.68
15.68
18.39
32.74
27.13
14.12
11.05
18.54
20.29
31.45
26.33
20.6
18.41
13.97
30.96
25.81
23.66
17.93
16.68
13.81
10.54
Lissocarpa_guianensis
Lissocarpa_kating
Lissocarpa_benthamii
Royena_zombensis
Royena_glabra
Royena_cordata
Royena_lucida1
Royena_lycioides
Royena_sp
Royena_whyteana
Euclea_pseudebenus
Euclea_crispa1
Euclea_divinorum
Euclea_sp1
Euclea_racemosa
Euclea_sp2
Euclea_natalensis
Euclea_undulata
Diospyros_maingayi
Diospyros_puncticulosa
Diospyros_pentamera
Diospyros_australis_NM
Diospyros_oubatchensis1
Diospyros_macrocarpa2
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Diospyros_margaretae
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Diospyros_bipindensis
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Diospyros_cooperi
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Diospyros_iturensis
Diospyros_mannii
Diospyros_fragrans
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Diospyros_cavalcantei
Diospyros_capreifolia
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Diospyros_carbonaria
Diospyros_vestita
Diospyros_ropourea
Diospyros_aculeata
Diospyros_boivinii
Diospyros_erythrosperma
Diospyros_velutipes
Diospyros_anosivolensis
Diospyros_leucocalyx
Diospyros_gracilipes1
Diospyros_dicorypheoides
Diospyros_kirkii
Diospyros_parvifolia
Diospyros_cinnamomoides
Diospyros_vescoi
Diospyros_fuscovelutina
Tetraclis_baronii
Diospyros_cf_clusiifolia
Diospyros_olacinoides
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Diospyros_stenocarpa
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Diospyros_myrtifolia
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Diospyros_sphaerosepala
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Maba_magnifolia
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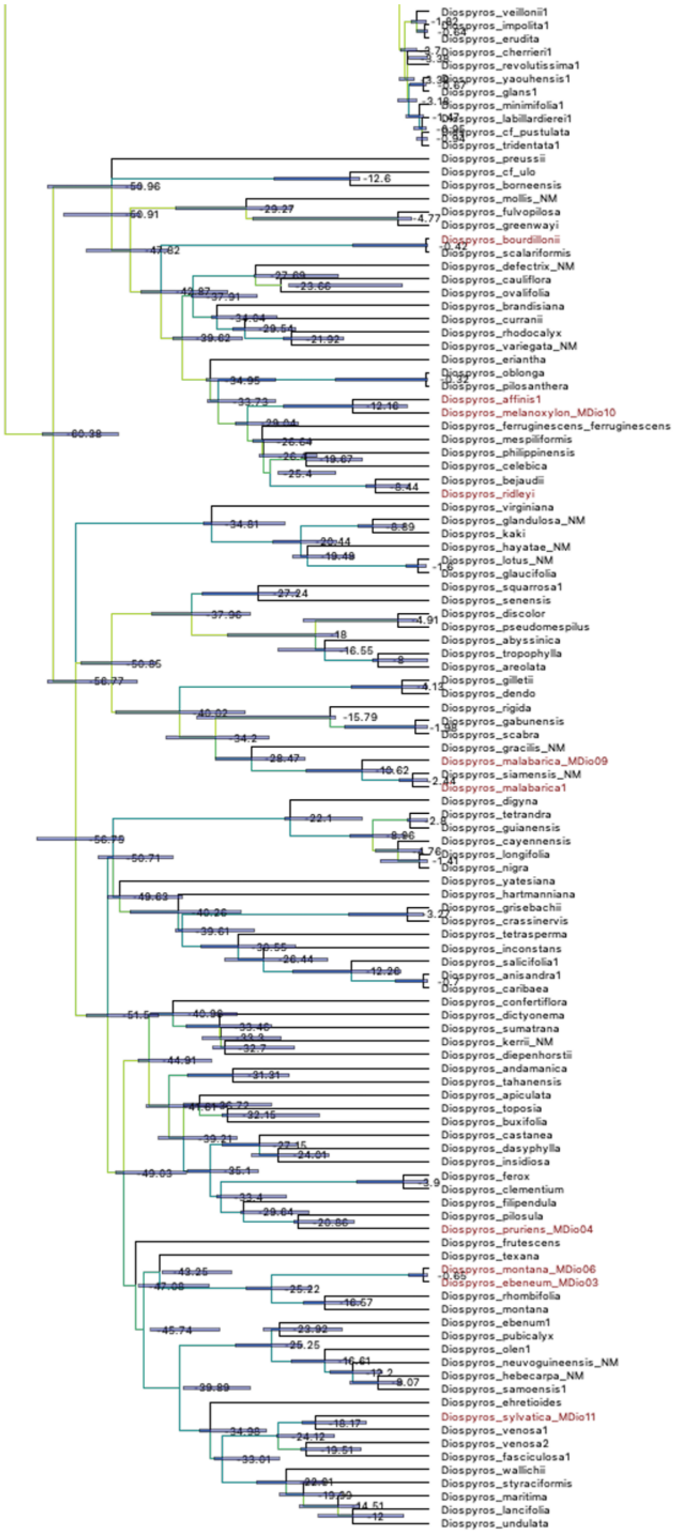
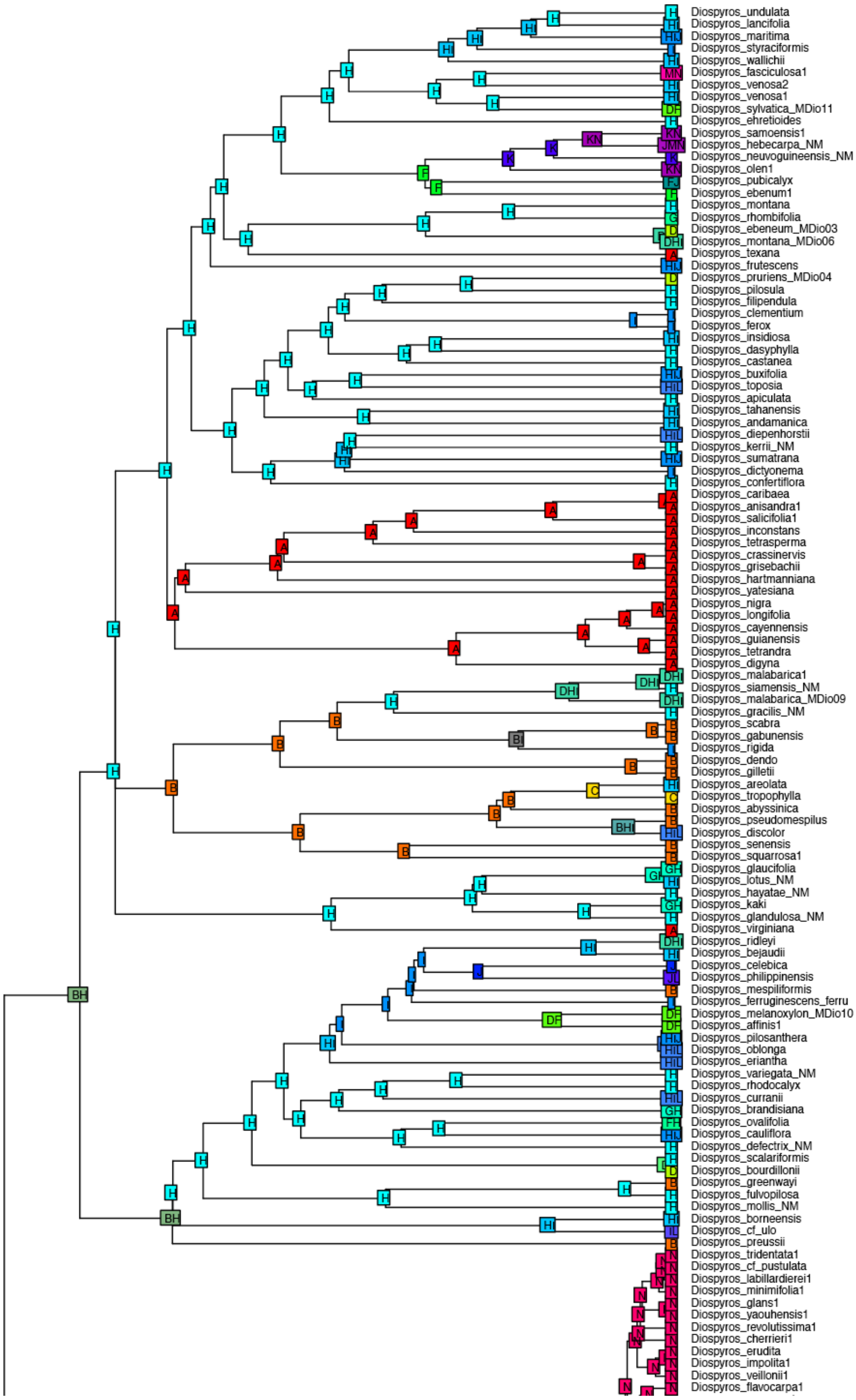


Figure 3.20: Time calibrated phylogeny of *Ebenaceae* focused on the genus *Diospyros* for 228 taxa.

Samples in red depict taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest.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Diospyros_venosa2
Diospyros_venosa1
Diospyros_sylvatica_MDio11
Diospyros_ehretioides
Diospyros_samoensis1
Diospyros_hebecarpa_NM
Diospyros_neuvoguineensis_NM
Diospyros_olen1
Diospyros_pubicalyx
Diospyros_ebenum1
Diospyros_montana
Diospyros_rhombifolia
Diospyros_ebeneum_MDio03
Diospyros_montana_MDio06
Diospyros_texana
Diospyros_frutescens
Diospyros_pruriens_MDio04
Diospyros_pilosula
Diospyros_filipendula
Diospyros_clementium
Diospyros_ferox
Diospyros_insidiosa
Diospyros_dasyphylla
Diospyros_castanea
Diospyros_buxifolia
Diospyros_toposia
Diospyros_apiculata
Diospyros_tahanensis
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Diospyros_diepenhorstii
Diospyros_kerrii_NM
Diospyros_sumatrana
Diospyros_dictyonema
Diospyros_confertiflora
Diospyros_caribaea
Diospyros_anisandra1
Diospyros_salicifolia1
Diospyros_inconstans
Diospyros_tetrasperma
Diospyros_crassinervis
Diospyros_grisebachii
Diospyros_hartmanniana
Diospyros_yatesiana
Diospyros_nigra
Diospyros_longifolia
Diospyros_cayennensis
Diospyros_guianensis
Diospyros_tetrandra
Diospyros_digyna
Diospyros_malabarica1
Diospyros_siamensis_NM
Diospyros_malabarica_MDio09
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Diospyros_scabra
Diospyros_gabunensis
Diospyros_rigida
Diospyros_dendo
Diospyros_gilletii
Diospyros_areolata
Diospyros_tropophylla
Diospyros_abyssinica
Diospyros_pseudomespilus
Diospyros_discolor
Diospyros_senensis
Diospyros_squarrosa1
Diospyros_glaucifolia
Diospyros_lotus_NM
Diospyros_hayatae_NM
Diospyros_kaki
Diospyros_glandulosa_NM
Diospyros_virginiana
Diospyros_ridleyi
Diospyros_bejaudii
Diospyros_celebica
Diospyros_philippinensis
Diospyros_mespiliformis
Diospyros_ferruginescens_ferru
Diospyros_melanoxylon_MDio10
Diospyros_affinis1
Diospyros_pilosanthera
Diospyros_oblonga
Diospyros_eriantha
Diospyros_variegata_NM
Diospyros_rhodocalyx
Diospyros_curranii
Diospyros_brandisiana
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Diospyros_defectrix_NM
Diospyros_scalariformis
Diospyros_bourdillonii
Diospyros_greenwayi
Diospyros_fulvopilosa
Diospyros_mollis_NM
Diospyros_borneensis
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Diospyros_preussii
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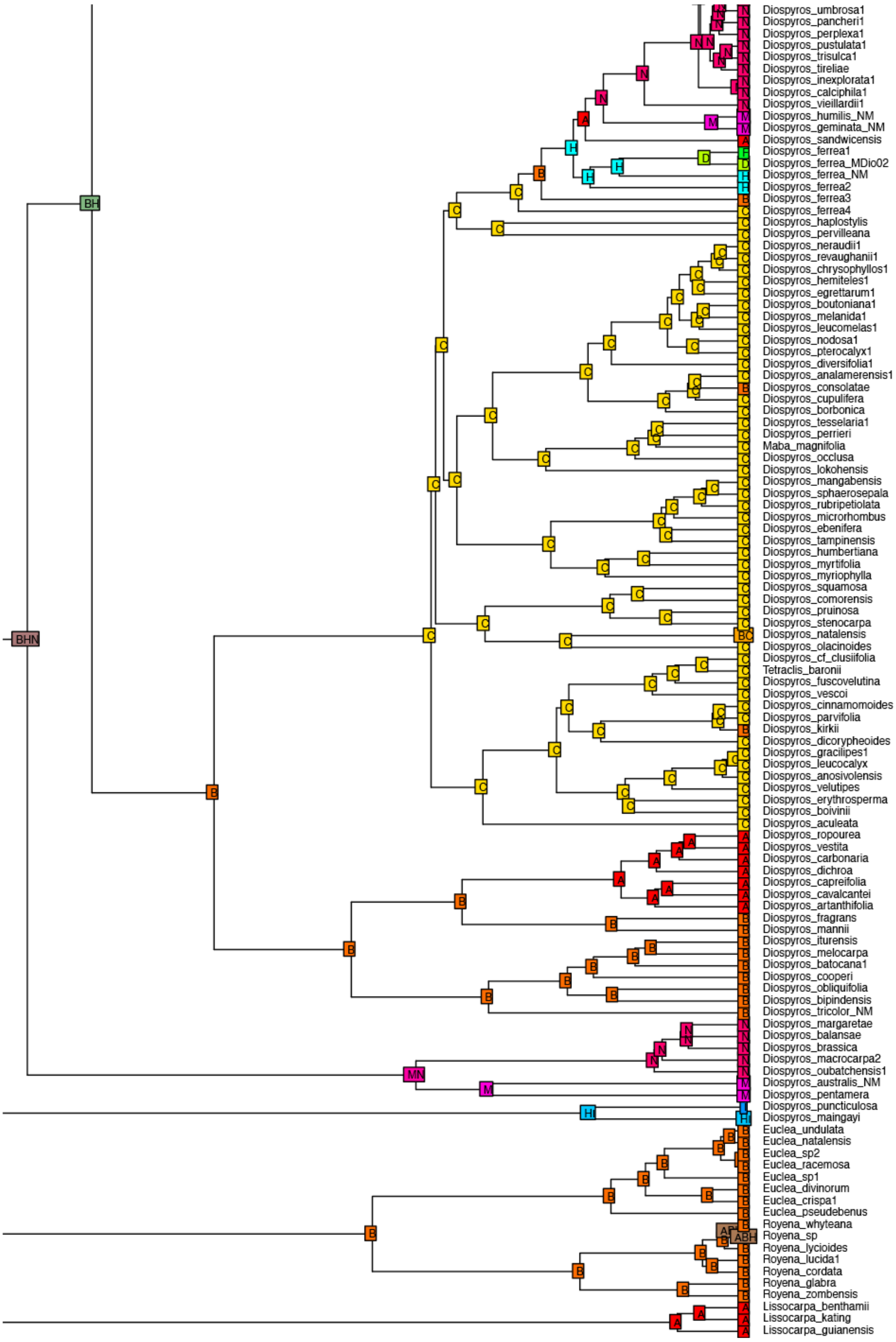

Figure 3.21: DEC+J ancestral area reconstruction for the family *Ebenaceae* focused on the genus *Diospyros*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Western Ghats (Light green), F=Sri Lanka (Neon green), H=Continental Asia (Light blue), I=Sunda Shelf (Indigo), J=Sahul Shelf (Royal blue). LnL value of -518.33. Clades listed in Table 3.4.

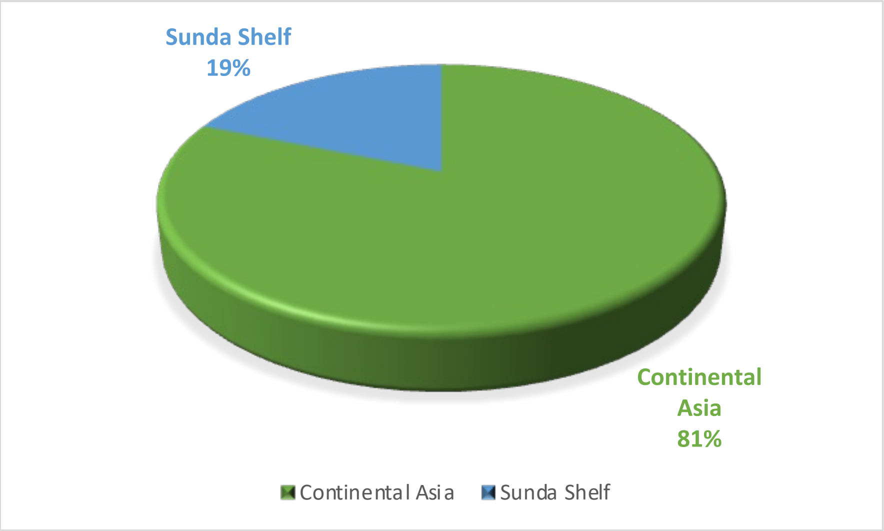

Figure 3.22: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Diospyros*, *Ebenaceae*.

Clade	**Taxa in clade**	**Minimum age (mya)**	**Area code**
Ebenaceae I	*Diospyros ferrea MDio02*	13.14	H
Ebenaceae II	*Diospyros bourdilonii*	42.87	H
Ebenaceae III	*Diospyros melanoxylon MDio10 and Diospyros affinis*	29.04	I
Ebenaceae IV	*Diospyros ridleyi*	8.44	HI
Ebenaceae V	*Diospyros malabarica1 and Diospyros malabarica MDio09*	28.47	H
Ebenaceae VI	*Diospyros pruriens MDio04*	20.86	H
Ebenaceae VII	*Diospyros ebneum MDio03, Diospyros montana MDio06*	25.22	H
Ebenaceae VIII	*Diospyros sylvatica MDio11*	18.17	H

Table 3.4: *Diospyros*, *Ebenaceae* table showing clade number, taxa found in each clade, their minimum age, and geographic origin.

3.3.6 *Lauraceae*

Maximum likelihood (Figure 3.23) and time calibrated (Figure 3.24) phylogenies were generated for 181 taxa of *Lauraceae* using ITS sequences (Chanderbali et al., 2001; Huang et al., 2016; Song et al., 2020). Seven clades (Table 3.5) were found endemic or native to the Ghats. All taxa in these clades were well supported. Clade I hosted the widespread species *Persea macrantha* now *Machilus glaucescens*, it was amongst taxa from America, Sri Lanka and Continental Asia. The clade had a minimum node age of 14.67 myr and showed origin signals from America, Sri Lanka and Continental Asia. Clade II had the Western Ghats and Sri Lankan native *Alseodaphne semecarpifolia*. The clade sits amongst taxa from Africa, Continental Asia, and the Sahul Shelf. It had a minimum node age of 21.7 myr and the DEC+J analysis (Figure 3.25) indicated Sahul Shelf origin. Clade II had the taxa *Litsea glabrata*, *Litsea sp_MSF24*, and *Litsea coriacea*, all Western Ghats endemics sister to taxa from China, Continental Asia, and the Sunda Shelf. The clade had a minimum node age of 10.07 myr and arrived from Continental Asia.

Clade IV hosted the Western Ghats endemic *Actinodaphne hookeri* now *Actinodaphne lanceolata.* The clade was sister to taxa from the Ghats and Continental Asia. It had a minimum node age of 9.83 million years and showed Continental Asian origin. Clade V had the samples *Neolitsea zeylanica* and *Neolitsea oblonga*. The samples are native to the Western Ghats but require taxonomic clarification. The clade sat amongst taxa from China and Continental Asia, it had a minimum node age of 5.76 myr and indicated a Continental Asian origin. Clade VI had the taxa *Litsea ligustrina* and *Litsea deccanensis*, native to the Western Ghats, Sri Lanka, and Continental Asia. The clade was amongst samples from China and Continental Asia. It had a minimum node age of 18.13 myr and showed Continental Asian origin.

Clade VII included the Western Ghats taxa *Cinnamomum sp MSF4*, *Cinnamomum sp MSF32*, *Cinnamomum sp MSF6*, *Cinnamomum sp MSF26* (PP 51), *Cinnamomum malabatrum MSF31*, the widespread *Cinnamomum iners MCin13*, and the Ghats and Continental Asian native *Cinnamomum macrocarpum MCin14.* Many of the taxa in this clade were field collected samples of different *Cinnamomum* species that require species determination. The clade was present amongst other *Cinnamomum* species from Continental Asia and the Sunda Shelf. It had a minimum node age of 11.3 million years and appears to have arrived from Continental Asia. The analyses suggest the arrival of *Lauraceae* taxa several times between c.5 and 22 million years ago. Taxa seem to have dispersed largely from the geographic regions of Continental Asia, with some arrivals from China and the Sahul Shelf.


Sextonia_pubescens
Mezilaurus_triunca
Anaueria_brasiliensis
Chlorocardium_rodiei
Chlorocardium_venenosum
Parasassafras_confertiflorum
Lindera_erythrocarpa
Lindera_umbellata
Lindera_benzoin
Actinodaphne_sesquipedalis
Actinodaphne_hookeri_MAct10
Neolitsea_cambodiana
Neolitsea_howii
Neolitsea_sericea
Neolitsea_zeylanica_MNeo03
Neolitsea_oblonga_MNeo01
Iteadaphne_sp_van_der_Werff_14360
Lindera_megaphylla
Litsea_lingustrina_MLit19
Litsea_deccanensis_MLit07
Laurus_nobilis
Litsea_coreana
Litsea_verticillata
Laureae_sp_Hyland_14912
Adenodaphne_uniflora
Litsea_auriculata
Litsea_glabrata_MLit06
Litsea_sp_MSF24
Litsea_coriacea_MLit04
Persea_meridensis
Persea_lingue
Persea_macarantha_MSF47
Dehaasia_incrassata
Apollonias_barbujana
Machilus_thunbergii
Persea_sp_14071
Phoebe_hungmoensis
Phoebe_formosana
Machilus_nanmu
Phoebe_zhennan
Alseodaphnopsis_hainanensis
Persea_americana
Alseodaphne_gigaphylla
Alseodaphne_semicarpifolia_MAls12
Alseodaphne_semecarpifolia
Sassafras_tzumu
Sassafras_albidum
Kuloa_ikonyokpe
Cinnamomum_javanicum
Cinnamomum_rhynchophyllum
Cinnamomum_baileyanum
Cinnamomum_laubatii
Cinnamomum_propinquum
Cinnamomum_oliveri
Cinnamomum_cordatum
Cinnamomum_austroyunnanense
Cinnamomum_tonkinense
Cinnamomum_multiflorum
Cinnamomum_kotoense
Cinnamomum_iners
Cinnamomum_grandifolium
Cinnamomum_bejolghota
Cinnamomum_macrocarpum_MCin14
Cinnamomum_sp_MSF4
Cinnamomum_sp_MSF32
Cinnamomum_sp_MSF6
Cinnamomum_iners_MCin13
Cinnamomum_sp_MSF26
Cinnamomum_malabatrum_MSF31
Cinnamomum_cuspidatum
Cinnamomum_longipetiolatum
Cinnamomum_chaogo
Cinnamomum_pittosporoides
Cinnamomum_sp_684
Cinnamomum_saxatile
Cinnamomum_reticulatum
Cinnamomum_insularimontanum
Cinnamomum_chekiangense
Cinnamomum_tenuifolium
Cinnamomum_daphnoides
Cinnamomum_doederleinii
Cinnamomum_aromaticum
Cinnamomum_sp_Lowry_et_al_4942
Cinnamomum_tamala
Cinnamomum_tsoi
Cinnamomum_celebicum
Cinnamomum_sintoc
Cinnamomum_sp_Huang_et_al_201310
Cinnamomum_subavenium
Cinnamomum_tsangii
Cinnamomum_austrosinense
Cinnamomum_pauciflorum
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Cinnamomum_okinawense
Cinnamomum_osmophloeum
Cinnamomum_appelianum

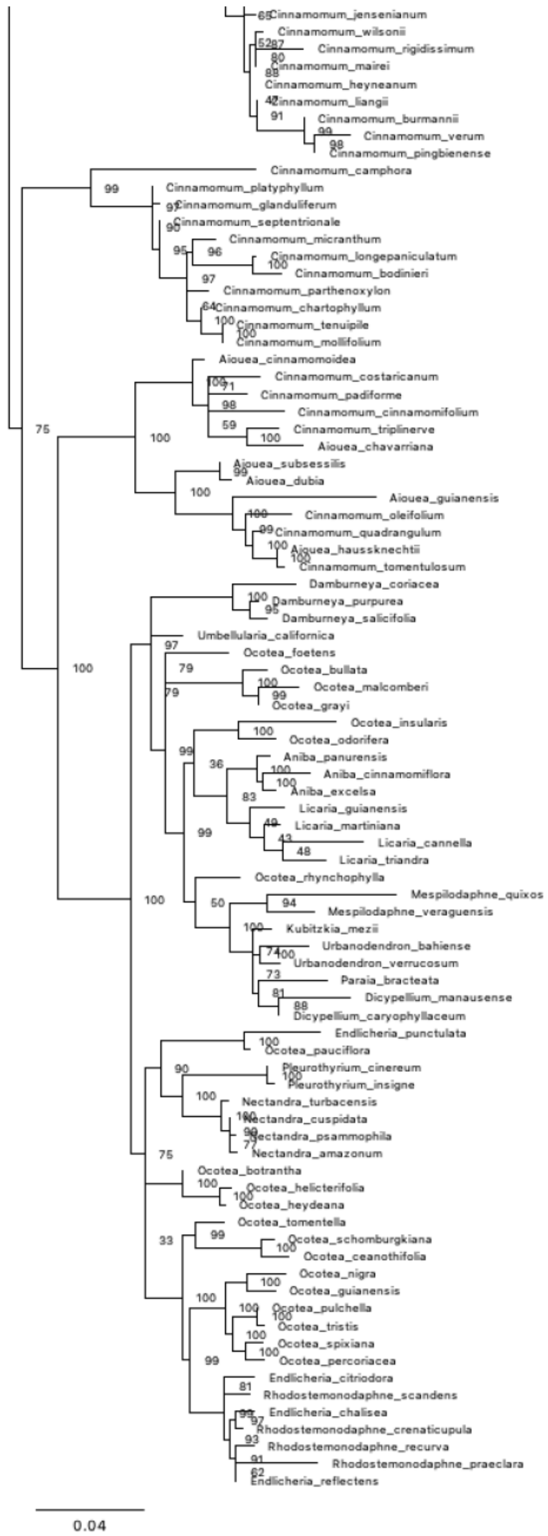
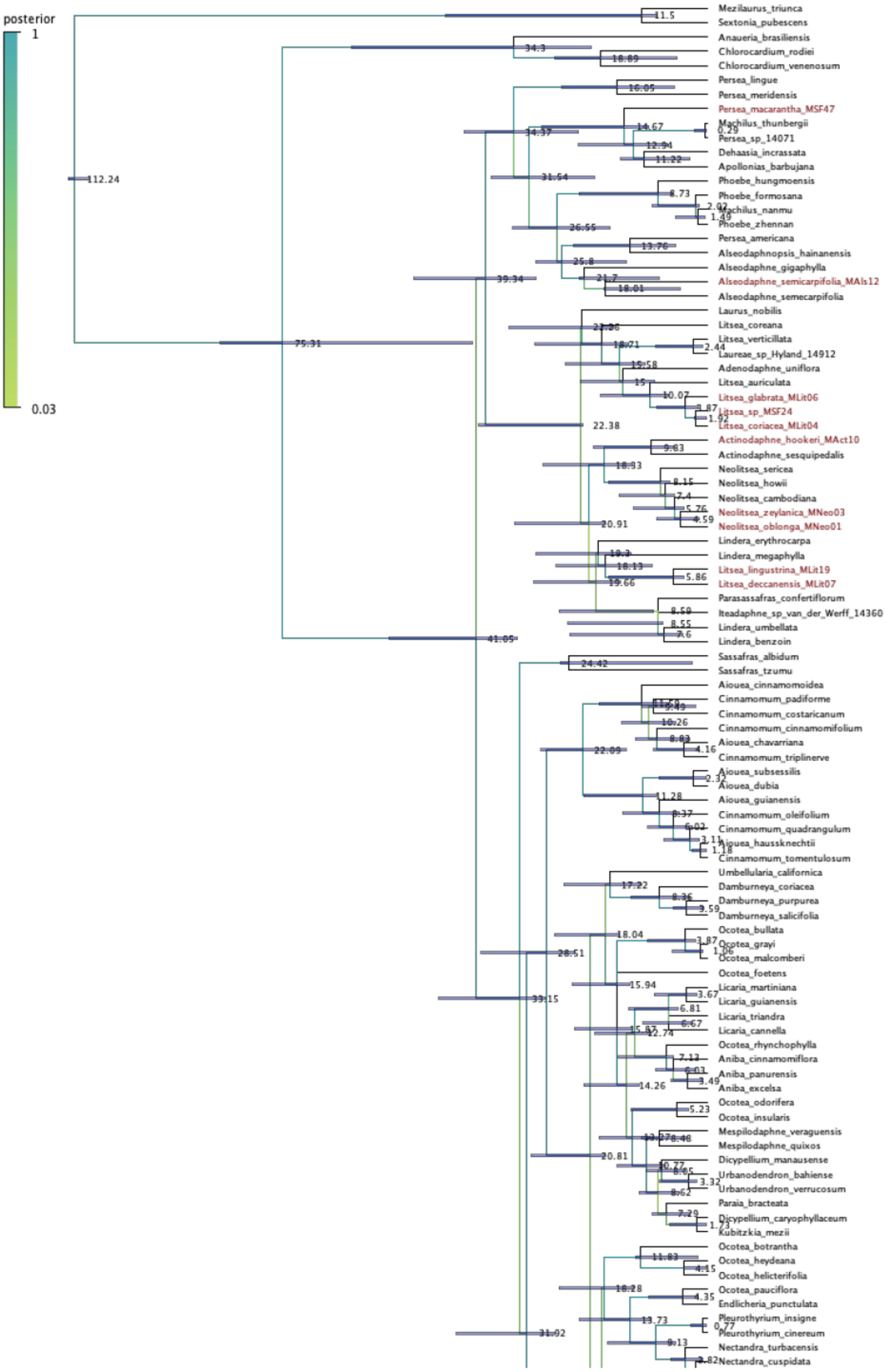


Figure 3.23: Maximum Likelihood phylogeny for the family *Lauraceae*.

The maximum likelihood phylogeny was generated for 182 taxa using IQTREE for ITS sequences. Samples in red indicate taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades.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39.34
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34.37
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26.55
25.8
22.38
20.91
33.15
28.51
31.92
11.5
Mezilaurus_triunca
Sextonia_pubescens
Anaueria_brasiliensis
18.89
Chlorocardium_rodiei
Chlorocardium_venenosum
16.05
Persea_lingue
Persea_meridensis
Persea_macarantha_MSF47
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0.29
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Persea_sp_14071
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Apollonias_barbujana
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2.02
1.49
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Phoebe_formosana
Machilus_nanmu
Phoebe_zhennan
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Persea_americana
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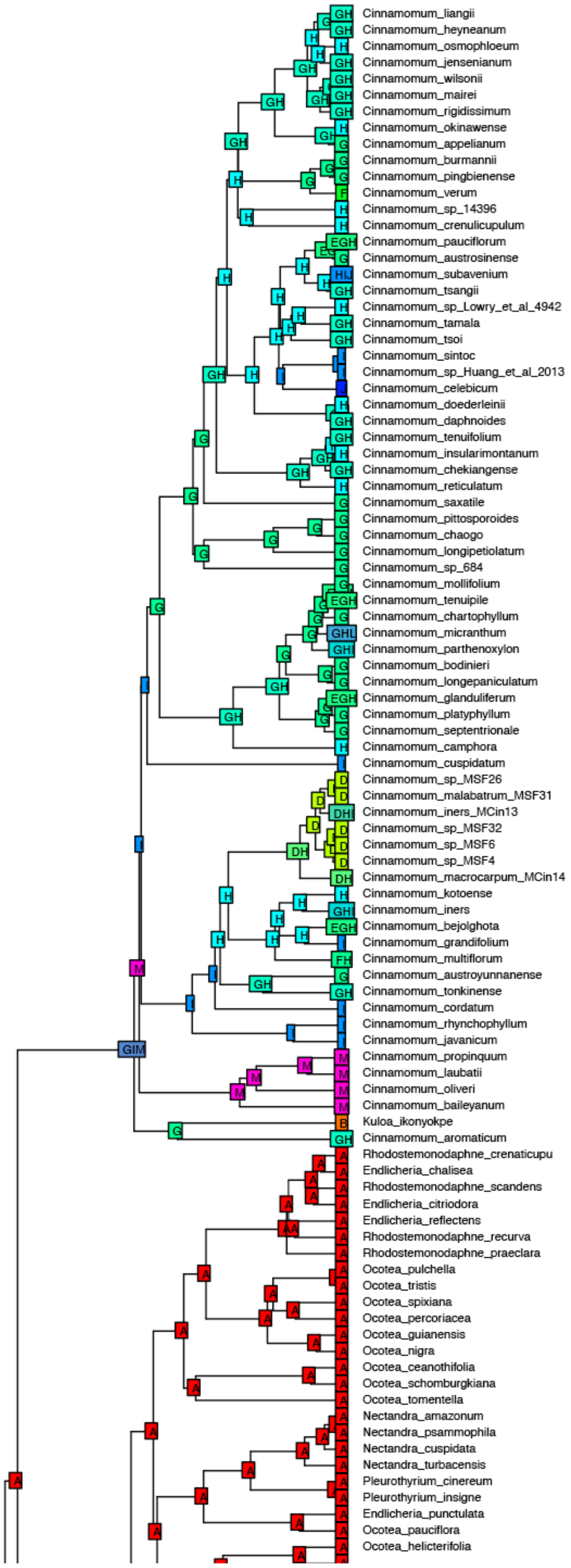
4.59
Actinodaphne_hookeri_MAct10
Actinodaphne_sesquipedalis
Neolitsea_sericea
Neolitsea_howii
Neolitsea_cambodiana
Neolitsea_zeylanica_MNeo03
Neolitsea_oblonga_MNeo01
19.3
18.13
19.66
5.86
Lindera_erythrocarpa
Lindera_megaphylla
Litsea_lingustrina_MLit19
Litsea_deccanensis_MLit07
8.59
8.55
7.6
Parasassafras_confertiflorum
Iteadaphne_sp_van_der_Werff_14360
Lindera_umbellata
Lindera_benzoin
24.42
Sassafras_albidum
Sassafras_tzumu
22.09
11.69
9.49
10.26
8.83
4.16
Aiouea_cinnamomoidea
Cinnamomum_padiforme
Cinnamomum_costaricanum
Cinnamomum_cinnamomifolium
Aiouea_chavarriana
Cinnamomum_triplinerve
2.32
11.28
9.37
6.02
3.11
1.18
Aiouea_subsessilis
Aiouea_dubia
Aiouea_guianensis
Cinnamomum_oleifolium
Cinnamomum_quadrangulum
Aiouea_haussknechtii
Cinnamomum_tomentulosum
17.22
8.36
3.59
Umbellularia_californica
Damburneya_coriacea
Damburneya_purpurea
Damburneya_salicifolia
18.04
3.87
1.06
Ocotea_bullata
Ocotea_grayi
Ocotea_malcomberi
15.94
Ocotea_foetens
3.67
6.81
6.67
15.87
12.74
Licaria_martiniana
Licaria_guianensis
Licaria_triandra
Licaria_cannella
7.13
6.03
3.49
14.26
Ocotea_rhynchophylla
Aniba_cinnamomiflora
Aniba_panurensis
Aniba_excelsa
5.23
Ocotea_odorifera
Ocotea_insularis
13.27
8.48
20.81
Mespilodaphne_veraguensis
Mespilodaphne_quixos
10.77
6.65
3.32
8.62
Dicypellium_manausense
Urbanodendron_bahiense
Urbanodendron_verrucosum
7.29
1.73
Paraia_bracteata
Dicypellium_caryophyllaceum
Kubitzkia_mezii
11.83
4.15
Ocotea_botrantha
Ocotea_heydeana
Ocotea_helicterifolia
18.28
4.35
Ocotea_pauciflora
Endlicheria_punctulata
13.73
0.77
Pleurothyrium_insigne
Pleurothyrium_cinereum
9.13
2.82
Nectandra_turbacensis
Nectandra_cuspidata

Figure 3.24: Time calibrated phylogeny of the family *Lauraceae* for 181 taxa.

Samples in red depict taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest.


Cinnamomum_liangii
Cinnamomum_heyneanum
Cinnamomum_osmophloeum
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Cinnamomum_wilsonii
Cinnamomum_mairei
Cinnamomum_rigidissimum
Cinnamomum_okinawense
Cinnamomum_appelianum
Cinnamomum_burmannii
Cinnamomum_pingbienense
Cinnamomum_verum
Cinnamomum_sp_14396
Cinnamomum_crenulicupulum
Cinnamomum_pauciflorum
Cinnamomum_austrosinense
Cinnamomum_subavenium
Cinnamomum_tsangii
Cinnamomum_sp_Lowry_et_al_4942
Cinnamomum_tamala
Cinnamomum_tsoi
Cinnamomum_sintoc
Cinnamomum_sp_Huang_et_al_2013
Cinnamomum_celebicum
Cinnamomum_doederleinii
Cinnamomum_daphnoides
Cinnamomum_tenuifolium
Cinnamomum_insularimontanum
Cinnamomum_chekiangense
Cinnamomum_reticulatum
Cinnamomum_saxatile
Cinnamomum_pittosporoides
Cinnamomum_chaogo
Cinnamomum_longipetiolatum
Cinnamomum_sp_684
Cinnamomum_mollifolium
Cinnamomum_tenuipile
Cinnamomum_chartophyllum
Cinnamomum_micranthum
Cinnamomum_parthenoxylon
Cinnamomum_bodinieri
Cinnamomum_longepaniculatum
Cinnamomum_glanduliferum
Cinnamomum_platyphyllum
Cinnamomum_septentrionale
Cinnamomum_camphora
Cinnamomum_cuspidatum
Cinnamomum_sp_MSF26
Cinnamomum_malabatrum_MSF31
Cinnamomum_iners_MCin13
Cinnamomum_sp_MSF32
Cinnamomum_sp_MSF6
Cinnamomum_sp_MSF4
Cinnamomum_macrocarpum_MCin14
Cinnamomum_kotoense
Cinnamomum_iners
Cinnamomum_bejolghota
Cinnamomum_grandifolium
Cinnamomum_multiflorum
Cinnamomum_austroyunnanense
Cinnamomum_tonkinense
Cinnamomum_cordatum
Cinnamomum_rhynchophyllum
Cinnamomum_javanicum
Cinnamomum_propinquum
Cinnamomum_laubatii
Cinnamomum_oliveri
Cinnamomum_baileyanum
Kuloa_ikonyokpe
Cinnamomum_aromaticum
Rhodostemonodaphne_crenaticupu
Endlicheria_chalisea
Rhodostemonodaphne_scandens
Endlicheria_citriodora
Endlicheria_reflectens
Rhodostemonodaphne_recurva
Rhodostemonodaphne_praeclara
Ocotea_pulchella
Ocotea_tristis
Ocotea_spixiana
Ocotea_percoriacea
Ocotea_guianensis
Ocotea_nigra
Ocotea_ceanothifolia
Ocotea_schomburgkiana
Ocotea_tomentella
Nectandra_amazonum
Nectandra_psammophila
Nectandra_cuspidata
Nectandra_turbacensis
Pleurothyrium_cinereum
Pleurothyrium_insigne
Endlicheria_punctulata
Ocotea_pauciflora
Ocotea_helicterifolia
GIM
M
G
A

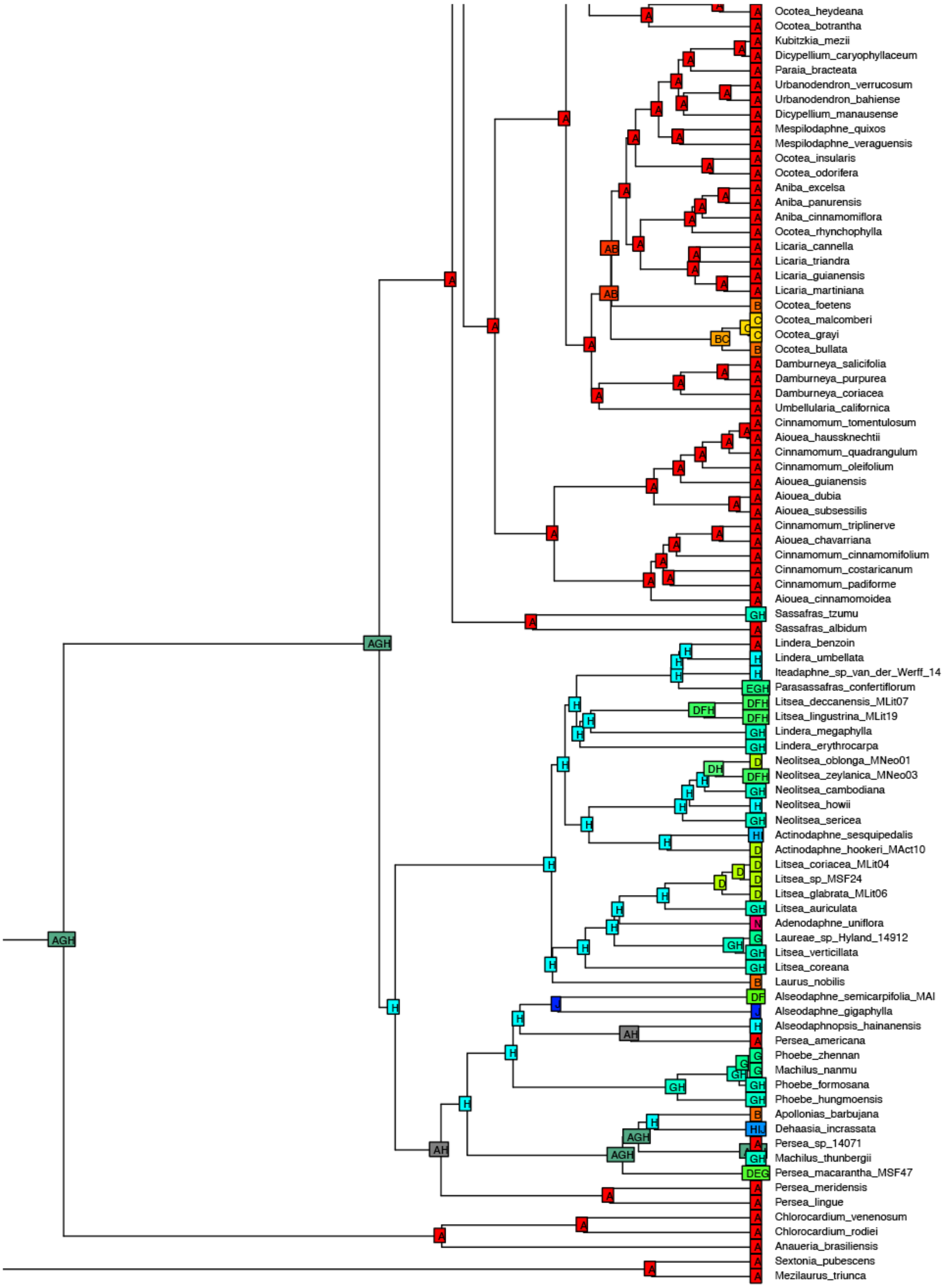


Figure 3.25: DEC+J ancestral area reconstruction for the family *Lauraceae*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Western Ghats (Light green), F=Sri Lanka (Neon green), G=China (Turquoise), H=Continental Asia (Light blue), I=Sunda Shelf (Indigo), J=Sahul Shelf (Royal blue), LnL value of -479.44. Clades listed in Table 3.5.

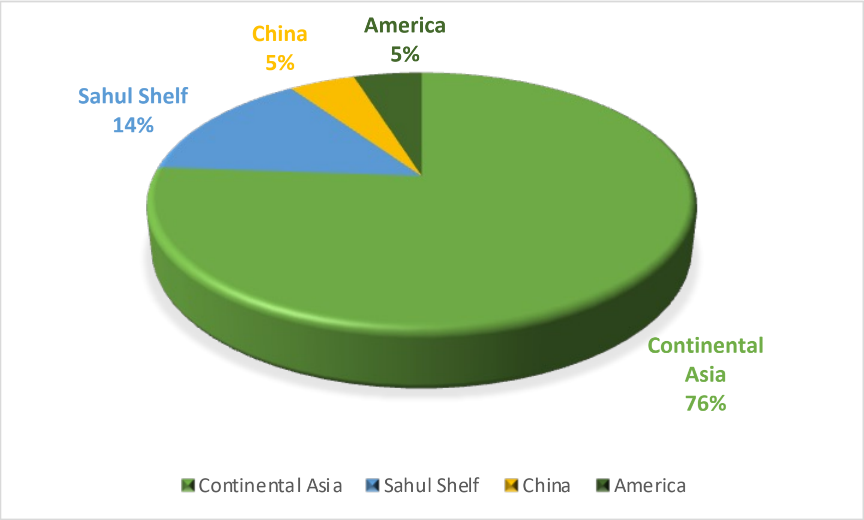


Figure 3.26: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Lauraceae*.

Clades	**Taxa in clades**	**Minimum age (mya)**	**Area code**
Lauraceae I	*Persea macrantha MSF47*	14.67	AGH
Lauraceae II	*Alseodaphne semecarpifolia MAls12*	21.7	J
Lauraceae III	*Litsea glabrata MLit06, Litsea sp MSF24, Litsea coriacea MLit04*	10.07	H
Lauraceae IV	*Actinodaphne hookeri MAct10*	9.83	H
Lauraceae V	*Neolitsea zeylanica MNeo03, Neolitsea oblonga MNeo01*	5.76	H
Lauraceae VI	*Litsea ligustrina MLit19, Litsea deccanensis MLit07*	18.13	H
Lauraceae VII	*Cinnamomum macrocarpum, Cinnamomum sp MSF4, Cinnamomum sp MSF32, Cinnamomum sp MSF6, Cinnamomum iners MCin13, Cinnamomum sp MSF26, Cinnamomum malabatrum MSF31*	11.3	H

Table 3.5: *Lauraceae* table showing clade number, taxa found in each clade, their minimum age, and geographic origin.

3.3.7 *Sapotaceae*

Maximum likelihood (Figure 3.27) and time calibrated (Figure 3.28) phylogenies were generated for 168 taxa of the family *Sapotaceae* using ITS sequences (Kumarage, 2016). Five clades (Table 3.6) of *Sapotaceae* in these phylogenies were found endemic or native to the Western Ghats. Clade I comprised of the taxa *Sideroxymon inerme*. The clade had a minimum node age of 16.97 myr and the DEC+J analysis (Figure 3.29) showed African origin. Clade II had the Western Ghats and Sri Lankan native *Mimusops elengi* (PP 100/53). This clade was amongst taxa from Africa, it had a minimum node age of 9.96 myr and also showed an African origin. Clade III included the taxa *Isonandra lanceolata2* (PP 84), it was amongst samples from the Sunda Shelf. The clade had a minimum node age of 26.8 myr and showed a Sunda Shelf signal.

Clade IV had the taxa – *Isonandra villosa*, *Isonandra perottetiana*, *Isonandra lanceolata_MSap04* and *Isonandra lanceolata_SL* (PP 100/54). The clade was surrounded by taxa from Sri Lanka and the Sunda Shelf. It had a minimum node age of 22.02 myr and showed a Sunda Shelf signal of geographic origin. Clade V included *Madhuca sp_MSF45*, a field collected sample endemic to the Western Ghats. The sample has potential to be either *Madhuca insignis* or *Madhuca nerifolia*, (PP 99/81). The clade was amongst samples from Sri Lanka and the Sunda Shelf, it had a minimum node age of 14.58 myr and showed a Sunda Shelf origin. The analyses suggest that the family *Sapotaceae* arrived to the Ghats between c.9 and 22 million years ago. The geographic signals indicate that the family came to the Ghats from either the Sunda Shelf or Africa (Figure).


Eberhardtia_aurata
Sarcosperma_laurinum
Sideroxylon_oxyacanthum
Xantolis_siamensis
Omphalocarpum_pachysteloides
Englerophytum_natalense
Poutera_firma
Pouteria_sp1
Pouteria_maclayana
Sideroxylon_salicifolium
Sideroxylon_repens
Sideroxylon_cubense
Sideroxylon_floribundum
Sideroxylon_capiri
Sideroxylon_foetidissimum
Sideroxylon_tepicense
Sideroxylon_mascatense
Argania_spinosa
Sideroxylon_inerme
Sideroxylon_marginatum
Sideroxylon_marmulano
Sideroxylon_saxorum
Sideroxylon_majus
Sideroxylon_betsimisarakum
Sideroxylon_wightianum
Sideroxylon_lycioides
Sideroxylon_tenax
Sideroxylon_reclinatum
Sideroxylon_lanuginosum
Sideroxylon_persimile
Nesoluma_polynesiacum
Sideroxylon_occidentale
Sideroxylon_americanum
Sideroxylon_obtusifolium
Sideroxylon_angustum
Sideroxylon_horridum
Sideroxylon_confertum
Sideroxylon_picardae
Sideroxylon_obovatum
Neolemonniera_clitandrifolia
Lecomtedoxa_klaineana
Northia_seychellana
Capurodendron_androyense
Baillonella_toxisperma
Vitellaria_paradoxa
Vitellariopsis_dispar
Vitellariopsis_marginata
Vitellariopsis_cuneata
Tieghemella_heckelii
Mimusops_obovata
Mimusops_elengi_MSF48
Mimusops_elengi_SL
Mimusops_zeyheri
Mimusops_caffra
Mimusops_comorensis
Autranella_congolensis
Labramia_costata
Labramia_mayottensis
Faucherea_parvifolia
Labourdonnaisia_calophylloides
Labourdonnaisia_revoluta
Manilkara_concolor
Manilkara_zapota
Manilkara_hexandra_SL
Manilkara_kauki
Letestua_durissima
Manilkara_obovata
Manilkara_discolor
Inhambanella_henriquesii
Palaquium_impressionervium
Palaquium_petiolare_SL
Palaquium_sp5_SL
Palaquium_sp4_SL
Palaquium_laevifolium_SL
Palaquium_grande_SL
Palaquium_sp3_SL
Palaquium_rubiginosum_SL
Palaquium_thwaitesii_SL
Palaquium_hinmolpedda_SL
Palaquium_canaliculatum_SL
Palaquium_pauciflorum_SL
Palaquium_clarkeanum
Palaquium_microphyllum
Palaquium_rufolanigerum
Palaquium_sumatranum
Palaquium_rostratum
Palaquium_rigidum
Palaquium_pseudorostratum
Palaquium_sp2
Palaquium_amboinense
Palaquium_formosanum
Palaquium_sericeum
Palaquium_dasyphyllum
Palaquium_galactoxylum
Palaquium_sp1
Palaquium_quercifolium
Aulandra_longifolia
Diploknema_oligomera
Palaquium_eriocalyx
Palaquium_oxleyanum
Palaquium_leiocarpum
Palaquium_cryptocarifolium
Palaquium_herveyi
Palaquium_beccarianum
Palaquium_maingayi
Palaquium_lobbianum
Palaquium_brassii
Palaquium_xanthochymum
Palaquium_calophyllum
Palaquium_obovatum
Palaquium_gutta
Palaquium_walsurifolium
Palaquium_hexandrum
Palaquium_ridleyi
Isonandra_montana_SL
Isonandra_perakensis
Madhuca_utilis
Madhuca_crassipes
Isonandra_lanceolata2

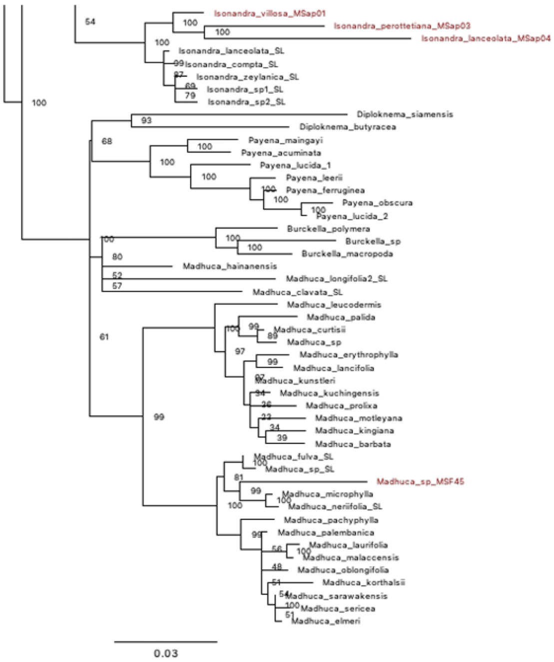
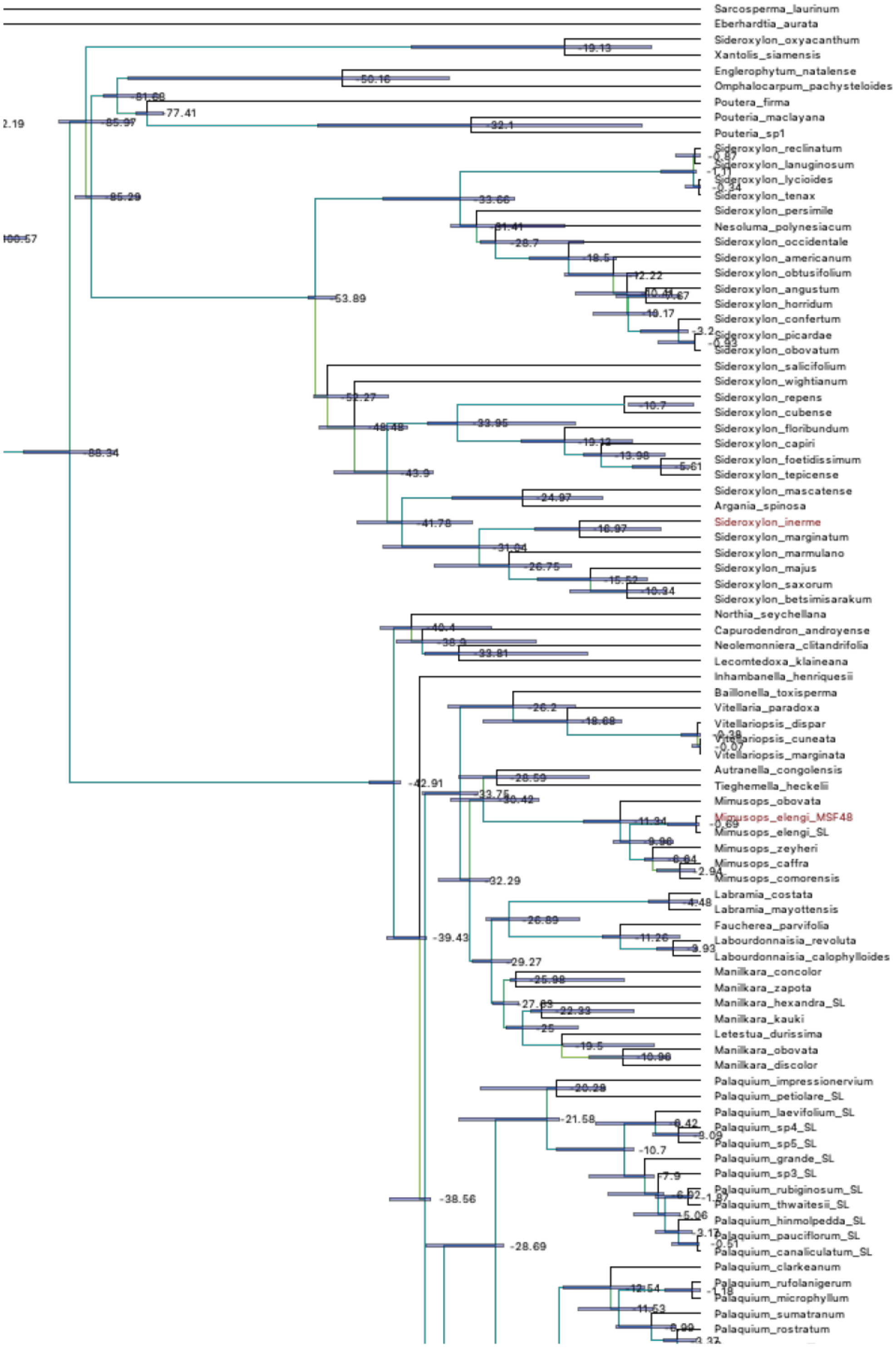


Figure 3.27: Maximum Likelihood phylogeny of the family *Sapotaceae*.

The maximum likelihood phylogeny was generated for 168 taxa using IQTREE for ITS sequences. Samples in red indicate taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades.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Sideroxylon_oxyacanthum
Xantolis_siamensis
Englerophytum_natalense
Omphalocarpum_pachysteloides
Pouteria_firma
Pouteria_maclayana
Pouteria_sp1
Sideroxylon_reclinatum
Sideroxylon_lanuginosum
Sideroxylon_lycioides
Sideroxylon_tenax
Sideroxylon_persimile
Nesoluma_polynesiacum
Sideroxylon_occidentale
Sideroxylon_americanum
Sideroxylon_obtusifolium
Sideroxylon_angustum
Sideroxylon_horridum
Sideroxylon_confertum
Sideroxylon_picardae
Sideroxylon_obovatum
Sideroxylon_salicifolium
Sideroxylon_wightianum
Sideroxylon_repens
Sideroxylon_cubense
Sideroxylon_floribundum
Sideroxylon_capiri
Sideroxylon_foetidissimum
Sideroxylon_tepicense
Sideroxylon_mascatense
Argania_spinosa
Sideroxylon_inerme
Sideroxylon_marginatum
Sideroxylon_marmulano
Sideroxylon_majus
Sideroxylon_saxorum
Sideroxylon_betsimisarakum
Northia_seychellana
Capurodendron_androyense
Neolemonniera_clitandrifolia
Lecomtedoxa_klaineana
Inhambanella_henriquesii
Baillonella_toxisperma
Vitellaria_paradoxa
Vitellariopsis_dispar
Vitellariopsis_cuneata
Vitellariopsis_marginata
Autranella_congolensis
Tieghemella_heckelii
Mimusops_obovata
Mimusops_elengi_MSF48
Mimusops_elengi_SL
Mimusops_zeyheri
Mimusops_caffra
Mimusops_comorensis
Labramia_costata
Labramia_mayottensis
Faucherea_parvifolia
Labourdonnaisia_revoluta
Labourdonnaisia_calophylloides
Manilkara_concolor
Manilkara_zapota
Manilkara_hexandra_SL
Manilkara_kauki
Letestua_durissima
Manilkara_obovata
Manilkara_discolor
Palaquium_impressionervium
Palaquium_petiolare_SL
Palaquium_laevifolium_SL
Palaquium_sp4_SL
Palaquium_sp5_SL
Palaquium_grande_SL
Palaquium_sp3_SL
Palaquium_rubiginosum_SL
Palaquium_thwaitesii_SL
Palaquium_hinmolpedda_SL
Palaquium_pauciflorum_SL
Palaquium_canaliculatum_SL
Palaquium_clarkeanum
Palaquium_rufolanigerum
Palaquium_microphyllum
Palaquium_sumatranum
Palaquium_rostratum
2.19
100.57
88.34
85.97
81.68
77.41
85.29
50.16
19.13
32.1
53.89
33.66
31.41
28.7
18.5
12.22
10.17
52.27
48.48
43.9
33.95
19.12
13.98
5.61
10.7
24.97
41.78
31.94
26.75
18.97
15.52
10.34
-42.91
40.4
38.9
33.81
26.2
18.68
-39.43
33.75
30.42
28.59
32.29
11.34
9.98
6.04
2.94
4.48
26.89
11.26
3.93
29.27
25.98
27.69
22.33
25
19.5
10.96
-38.56
20.28
-21.58
8.42
3.09
-10.7
7.9
6.06
3.17
-28.69
12.54
11.53
6.09
3.37

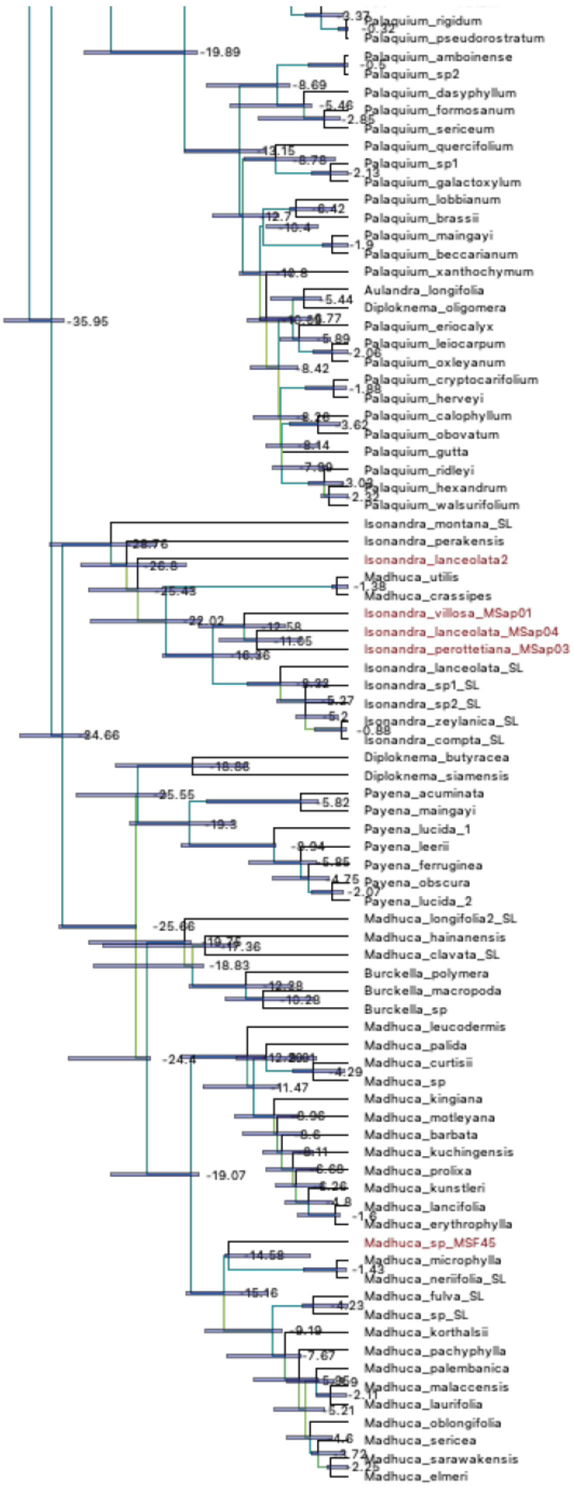


Figure 3.28: Time calibrated phylogeny of the family *Sapotaceae* for 167 taxa.

Samples in red depict taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest.


Madhuca_elmeri
Madhuca_sarawakensis
Madhuca_sericea
Madhuca_oblongifolia
Madhuca_laurifolia
Madhuca_malaccensis
Madhuca_palembanica
Madhuca_pachyphylla
Madhuca_korthalsii
Madhuca_sp_SL
Madhuca_fulva_SL
Madhuca_neriifolia_SL
Madhuca_microphylla
Madhuca_sp_MSF45
Madhuca_erythrophylla
Madhuca_lancifolia
Madhuca_kunstleri
Madhuca_prolixa
Madhuca_kuchingensis
Madhuca_barbata
Madhuca_motleyana
Madhuca_kingiana
Madhuca_sp
Madhuca_curtisii
Madhuca_palida
Madhuca_leucodermis
Burckella_sp
Burckella_macropoda
Burckella_polymera
Madhuca_clavata_SL
Madhuca_hainanensis
Madhuca_longifolia2_SL
Payena_lucida_2
Payena_obscura
Payena_ferruginea
Payena_leerii
Payena_lucida_1
Payena_maingayi
Payena_acuminata
Diploknema_siamensis
Diploknema_butyracea
Isonandra_compta_SL
Isonandra_zeylanica_SL
Isonandra_sp2_SL
Isonandra_sp1_SL
Isonandra_lanceolata_SL
Isonandra_perottetiana_MSap03
Isonandra_lanceolata_MSap04
Isonandra_villosa_MSap01
Madhuca_crassipes
Madhuca_utilis
Isonandra_lanceolata2
Isonandra_perakensis
Isonandra_montana_SL
Palaquium_walsurifolium
Palaquium_hexandrum
Palaquium_ridleyi
Palaquium_gutta
Palaquium_obovatum
Palaquium_calophyllum
Palaquium_herveyi
Palaquium_cryptocarifolium
Palaquium_oxleyanum
Palaquium_leiocarpum
Palaquium_eriocalyx
Diploknema_oligomera
Aulandra_longifolia
Palaquium_xanthochymum
Palaquium_beccarianum
Palaquium_maingayi
Palaquium_brassii
Palaquium_lobbianum
Palaquium_galactoxylum
Palaquium_sp1
Palaquium_quercifolium
Palaquium_sericeum
Palaquium_formosanum
Palaquium_dasyphyllum
Palaquium_sp2
Palaquium_amboinense
Palaquium_pseudorostratum
Palaquium_rigidum
Palaquium_rostratum
Palaquium_sumatranum
Palaquium_microphyllum
Palaquium_rufolanigerum
Palaquium_clarkeanum
Palaquium_canaliculatum_SL
Palaquium_pauciflorum_SL

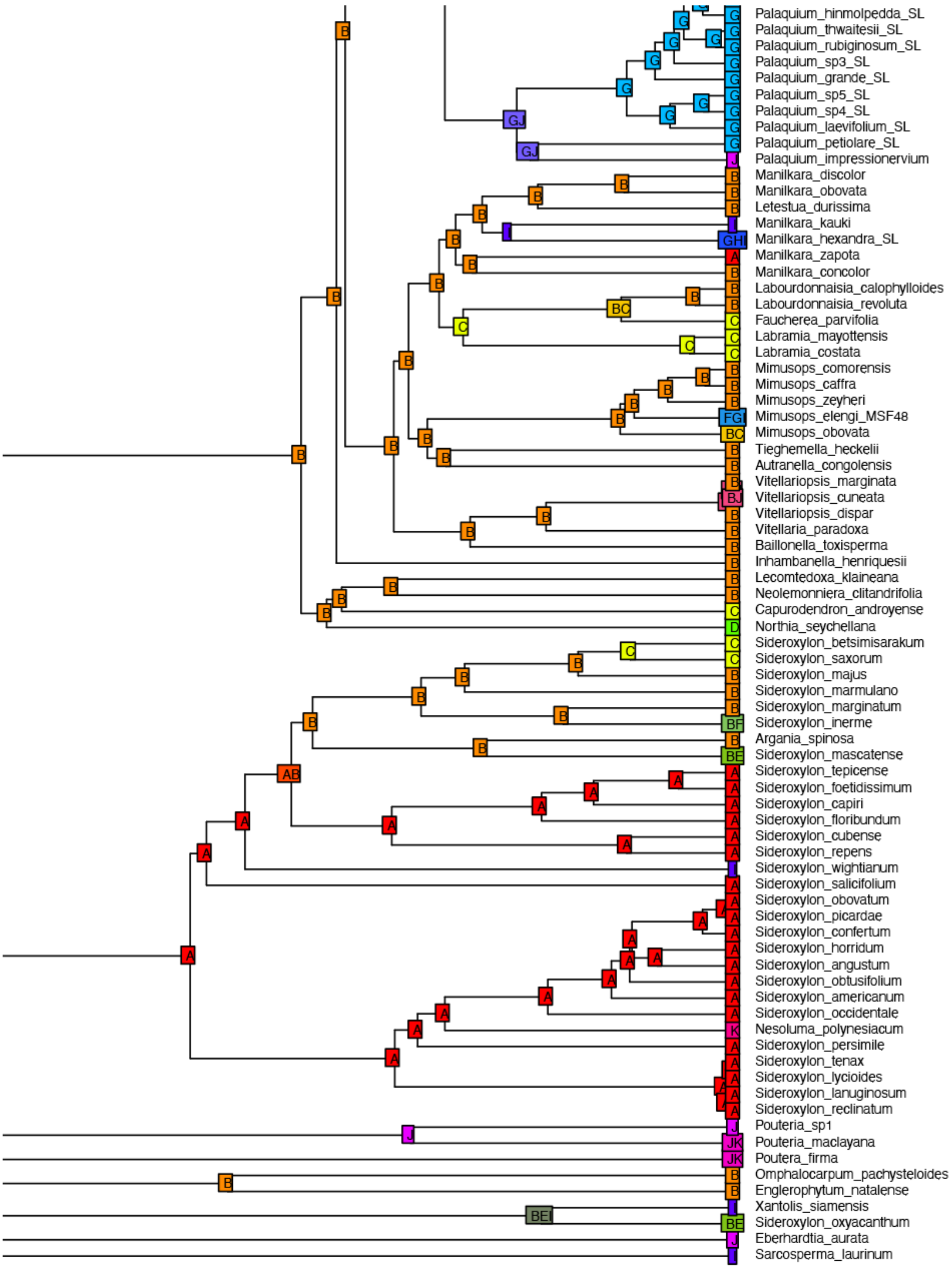


Figure 3.29: DEC+J ancestral area reconstruction for the family *Sapotaceae*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Seychelles (Light green), E=Middle East (Green), F=Western Ghats (Neon green), G=Sri Lanka (Light blue), H=Himalayas (Royal blue), I=Continental Asia (Purple), J=Sunda Shelf (Magenta), K=Sahul Shelf (Pink). LnL value of -294.19. Clades listed in Table 3.6.

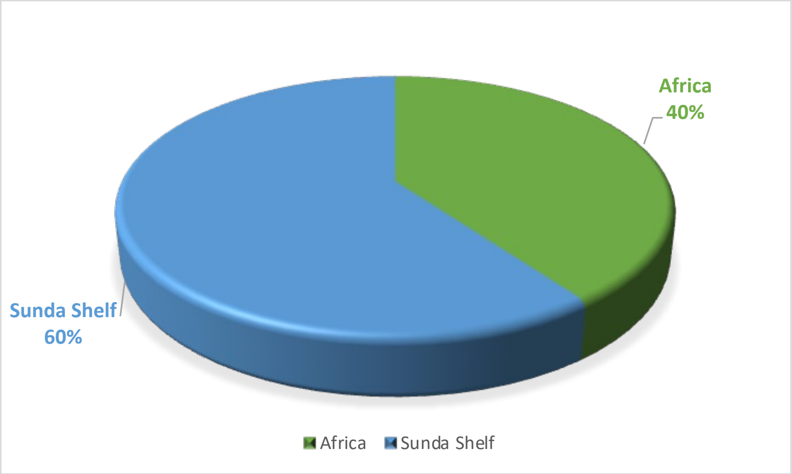


Figure 3.30: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Sapotaceae*.

Clade	**Taxa in clade**	**Minimum age (mya)**	**Area code**
Sapotaceae I	*Sideroxylon inerme*	16.97	B
Sapotaceae II	*Mimusops elengi MSF48*	9.96	B
Sapotaceae III	*Isonandra lanceolata2*	26.8	J
Sapotaceae IV	*Isonandra villosa MSap01, Isonandra perottetiana MSap03, Isonandra lanceolata MSap04, Isonandra lanceolata SL*	22.02	J
Sapotaceae V	*Madhuca sp MSF45*	14.58	J

Table 3.6: *Sapotaceae* table showing clade number, taxa found in each clade, their minimum age, and geographic origin.

3.3.8 *Zingiberaceae*

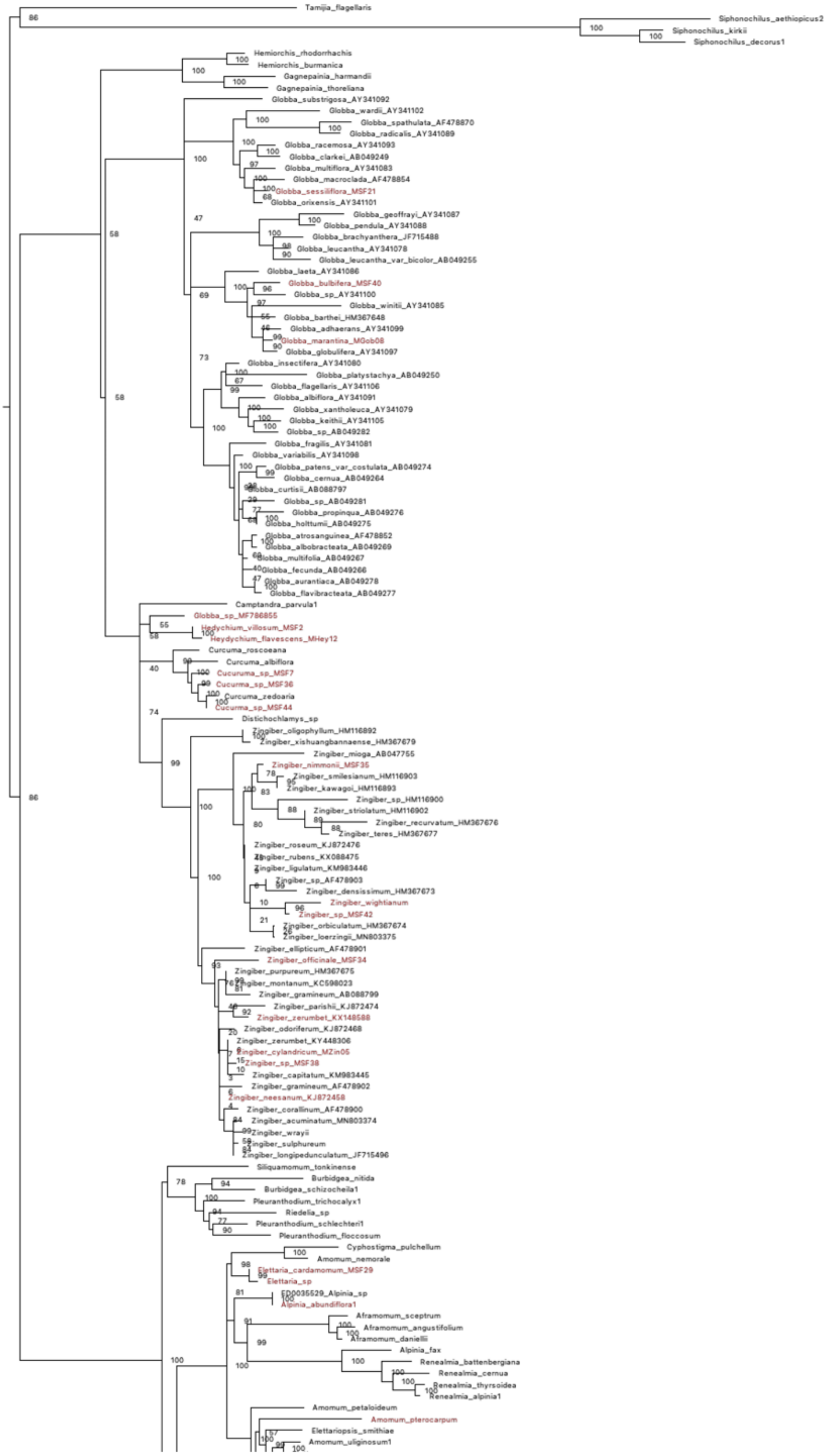
Maximum likelihood (Figure 3.31) and time calibrated (Figure 3.32) phylogenies were generated for 238 taxa of *Zingiberaceae* using the loci matK (Kumarage, 2016). 16 clades (Table 3.7) were found with taxa native or endemic to the Western Ghats. Most of these clades were well supported in the phylogenies unless otherwise specified. Clade I hosted the Western Ghats and Continental Asian native *Globba sessiliflora*. The clade was well supported and amongst taxa from Continental Asia and Sri Lanka. It had a minimum node age of 4.11 myr, DEC+J analysis (Figure 3.33)showed a Continental Asian origin. Clade II had the taxa *Globba bulbifera MSF40*, a field collected sample from the Western Ghats, found amongst taxa from China and Continental Asia. The clade had a minimum node age of 4.04 myr and indicated Continental Asian origin.

Clade III hosted the widespread taxa *Globba marantina MGob08*, it sat amongst taxa from Continental Asia. It had a minimum node age of 4.27 myr and indicated Continental Asian arrival. Clade IV hosted the widespread taxa *Hedychium flavescens*, *Hedychium villosum*, and Globba *sp MF786855*, this was not a well supported clade (PP 58). It had a minimum node age of 18.07 myr and indicated Continental Asian origin. Clade V included the field collected taxa *Curcuma sp MSF7*, *Curcuma sp MSF36*, and *Curcuma sp MSF44*. These taxa were well supported but require species level determination. They were placed amongst taxa from the Western Ghats, Sri Lanka, and Continental Asia. The clade had a minimum node age of 14.74 myr and indicated Continental Asian origin. Clade VI included the Western Ghats and Sri Lankan endemics *Zingiber sp MSF42* and *Zingiber wightianum*. The clade was not well supported and was placed amongst taxa from China and the Sunda Shelf. It had a minimum node age of 2.59 million years and arrived to the Ghats from China.

Clade VII included the taxa *Zingiber nimmonii* (PP 78), its placed amongst taxa from the Himalayas and Continental Asia. It had a minimum node age of 0.82 myr and showed Continental Asian origin. Clade VIII had the widespread species *Zingiber officinale*, the clade was well supported and placed amongst samples from China and Continental Asia. It had a minimum node age of 12.16 myr and appears to have arrived from China. Clade IX had the widespread taxa *Zingiber zerumbet*, it was placed amongst taxa from China, Continental Asia, and the Sunda Shelf. A taxonomically identical sample exists elsewhere in the tree, name clarification is necessary. The clade had a minimum node age of 5.12 myr and potentially originated from China, Continental Asia, or the Sunda Shelf. Clade X had the taxa *Zingiber neesanum* (PP 6), this was not a resolved clade. The clade placed amongst taxa from Continental Asia and the Sunda Shelf. It had a minimum node age of 5.31 myr and showed Sunda Shelf origin.

Clade XI had the taxa *Zingiber cylindricum MZin05* and *Zingiber sp MSF38*, this was an unresolved clade that sat amongst taxa from China, the Himalayas, and Continental Asia. It had a minimum node age of 5.31 myr and indicated Sunda Shelf origin. Clade XII was well resolved had the taxa *Alpinia abundiflora1*, *Elettaria sp*, and Elettaria *cardamomum MSF29*, it sat amongst taxa from Sri Lanka, China, and Continental Asia. The clade had a minimum node age of 16.8 myr and had a geographic signal from Sri Lanka. Clade XIII had the Western Ghats and Sri Lankan taxa *Amomum pterocarpum* (PP 57), the clade was poorly supported and placed amongst taxa from China and the Sunda Shelf. It had a minimum node age of 5.6 myr and appears to have originated from Sri Lanka. Clade XIV was well supported and had two field collected samples *Alpinia sp MSF43* and *Alpinia sp MSF25*, that sat amongst taxa from China. It had a minimum node age of 3.62 my and originated from China.

Clade XV had the taxa *Amomum sp MSF23* (PP 100) it placed amongst taxa from Sri Lanka and the Sunda Shelf. It had a minimum node age of 4.24 myr and showed Sri Lankan origin. Clade XVI had the well supported taxa *Amomum fulviceps* a Western Ghats and Sri Lankan taxa. It had a minimum node age of 0.47 myr and showed Sri Lankan origin. The analyses indicate that the family *Zingiberaceae* dispersed to the Ghats several times between c.0.4and 19million years ago. Taxa of *Zingiberaceae* have been dispersing to the Ghats until quite recently predominantly from the regions of Continental Asia, Sri Lanka, and China.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Gagnepainia_thoreliana
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Globba_spathulata_AF478870
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Globba_sessiliflora_MSF21
Globba_orixensis_AY341101
Globba_geoffrayi_AY341087
Globba_pendula_AY341088
Globba_brachyanthera_JF715488
Globba_leucantha_AY341078
Globba_leucantha_var_bicolor_AB049255
Globba_laeta_AY341086
Globba_bulbifera_MSF40
Globba_sp_AY341100
Globba_winitii_AY341085
Globba_barthei_HM367648
Globba_adhaerans_AY341099
Globba_marantina_MGob08
Globba_globulifera_AY341097
Globba_insectifera_AY341080
Globba_platystachya_AB049250
Globba_flagellaris_AY341106
Globba_albiflora_AY341091
Globba_xantholeuca_AY341079
Globba_keithii_AY341105
Globba_sp_AB049282
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Globba_variabilis_AY341098
Globba_patens_var_costulata_AB049274
Globba_cernua_AB049264
Globba_curtisii_AB088797
Globba_sp_AB049281
Globba_propinqua_AB049276
Globba_holttumii_AB049275
Globba_atrosanguinea_AF478852
Globba_albobracteata_AB049269
Globba_multifolia_AB049267
Globba_fecunda_AB049266
Globba_aurantiaca_AB049278
Globba_flavibracteata_AB049277
Camptandra_parvula1
Globba_sp_MF786855
Hedychium_villosum_MSF2
Heydychium_flavescens_MHey12
Curcuma_roscoeana
Curcuma_albiflora
Cucuruma_sp_MSF7
Cucurma_sp_MSF36
Curcuma_zedoaria
Cucurma_sp_MSF44
Distichochlamys_sp
Zingiber_oligophyllum_HM116892
Zingiber_xishuangbannaense_HM367679
Zingiber_mioga_AB047755
Zingiber_nimmonii_MSF35
Zingiber_smilesianum_HM116903
Zingiber_kawagoi_HM116893
Zingiber_sp_HM116900
Zingiber_striolatum_HM116902
Zingiber_recurvatum_HM367676
Zingiber_teres_HM367677
Zingiber_roseum_KJ872476
Zingiber_rubens_KX088475
Zingiber_ligulatum_KM983446
Zingiber_sp_AF478903
Zingiber_densissimum_HM367673
Zingiber_wightianum
Zingiber_sp_MSF42
Zingiber_orbiculatum_HM367674
Zingiber_loerzingii_MN803375
Zingiber_ellipticum_AF478901
Zingiber_officinale_MSF34
Zingiber_purpureum_HM367675
Zingiber_montanum_KC598023
Zingiber_gramineum_AB088799
Zingiber_parishii_KJ872474
Zingiber_zerumbet_KX148588
Zingiber_odoriferum_KJ872468
Zingiber_zerumbet_KY448306
Zingiber_cylandricum_MZin05
Zingiber_sp_MSF38
Zingiber_capitatum_KM983445
Zingiber_gramineum_AF478902
Zingiber_neesanum_KJ872458
Zingiber_corallinum_AF478900
Zingiber_acuminatum_MN803374
Zingiber_wrayii
Zingiber_sulphureum
Zingiber_longipedunculatum_JF715496
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Burbidgea_nitida
Burbidgea_schizocheila1
Pleuranthodium_trichocalyx1
Riedelia_sp
Pleuranthodium_schlechteri1
Pleuranthodium_floccosum
Cyphostigma_pulchellum
Amomum_nemorale
Elettaria_cardamomum_MSF29
Elettaria_sp
ED0035529_Alpinia_sp
Alpinia_abundiflora1
Aframomum_sceptrum
Aframomum_angustifolium
Aframomum_daniellii
Alpinia_fax
Renealmia_battenbergiana
Renealmia_cernua
Renealmia_thyrsoidea
Renealmia_alpinia1
Amomum_petaloideum
Amomum_pterocarpum
Elettariopsis_smithiae
Amomum_uliginosum1


100
Elettariopsis_sp
99
Elettariopsis_stenosiphon
89
100
Elettariopsis_kerbyi
Amomum_putrescens
Amomum_sericeum
4389
Amomum_glabrum2
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Amomum_menglaense
39
Amomum_austrosinense
78
53
Amomum_queenslandicum
100
Zingiber_engganoensis_KT026200
46
Amomum_maximum
44
Amomum_purpureorubrum
Alpinia_conchigera
100
Alpinia_galanga2
60
Alpinia_rafflesiana
63
Alpinia_nigra
100
Alpinia_bilamellata
Alpinia_carolinensis
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Alpinia_eremochlamys
100
Alpinia_aenea
97
Alpinia_monopleura
100
Alpinia_coeruleoviridis
100
Alpinia_cylindrocephala
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Alpinia_ligulata1
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Alpinia_nieuwenhuizii
99
Alpinia_rubricaulis
98
Alpinia_argentea
100
Alpinia_warburgii
Alpinia_rosea
100
Alpinia_foxworthyi
100
100
Alpinia_brevilabris
100
Alpinia_flabellata
99
Alpinia_sibuyanensis
87
Alpinia_vulcanica
100
99
Alpinia_oxyphylla
Alpinia_latilabris
100
Alpinia_hookeriana
86
Alpinia_sp_MSF43
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Alpinia_sp_MSF25
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Alpinia_rugosa
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91
Alpinia_calcarata
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Alpinia_nutans
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Alpinia_polyantha
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Alpinia_shimadae
60
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Alpinia_mutica
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Alpinia_zerumbet
89
Alpinia_coriacea
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Alpinia_pumila
Alpinia_japonica
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Alpinia_pricei
Alpinia_formosana
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Alpinia_intermedia
66
Alpinia_tonkinensis
95
Alpinia_guangdongensis
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Alpinia_maclurei
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Amomum_aff__paratsaoko
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Amomum_coriandriodorum
Amomum_pierreanum2
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Amomum_xanthophlebium
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Etlingera_elatior1
Etlingera_triorgyalis
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Leptosolena_haenkei
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87
Alpinia_purpurata
88
Alpinia_vittata
88
100
98
Alpinia_oceanica
Vanoverberghia_sepulchrei
79
Alpinia_arctiflora
Alpinia_modesta
83
Alpinia_caerulea
80
Alpinia_arundelliana
82
Alpinia_luteocarpa
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97
Alpinia_elegans
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Geocharis_sp2
100
Geocharis_sp1
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Hornstedtia_hainanensis
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Amomum_lappaceum1
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Amomum_centrocephalum1
Amomum_staminidivum
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Amomum_quadratolaminare
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Elettariopsis_sp5
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Amomum_sp2
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Amomum_villosum
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Amomum_uliginosum2
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Amomum_krervanh3
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Amomum_krervanh2
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Amomum_hastilabium1
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Amomum_pseudofoetens
Amomum_laxesquamosum
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Amomum_compactum2
Amomum_oligophyllum
81
Amomum_hastilabium2
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Amomum_sp9
98
Amomum_yunnanense
93
Amomum_koenigii
Amomum_propinquum
99
100
Amomum_sp6
100
Amomum_sp5
95
Amomum_aculeatum
81
Amomum_mentawaiense
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Amomum_masticatorium
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Amomum_graminifolium
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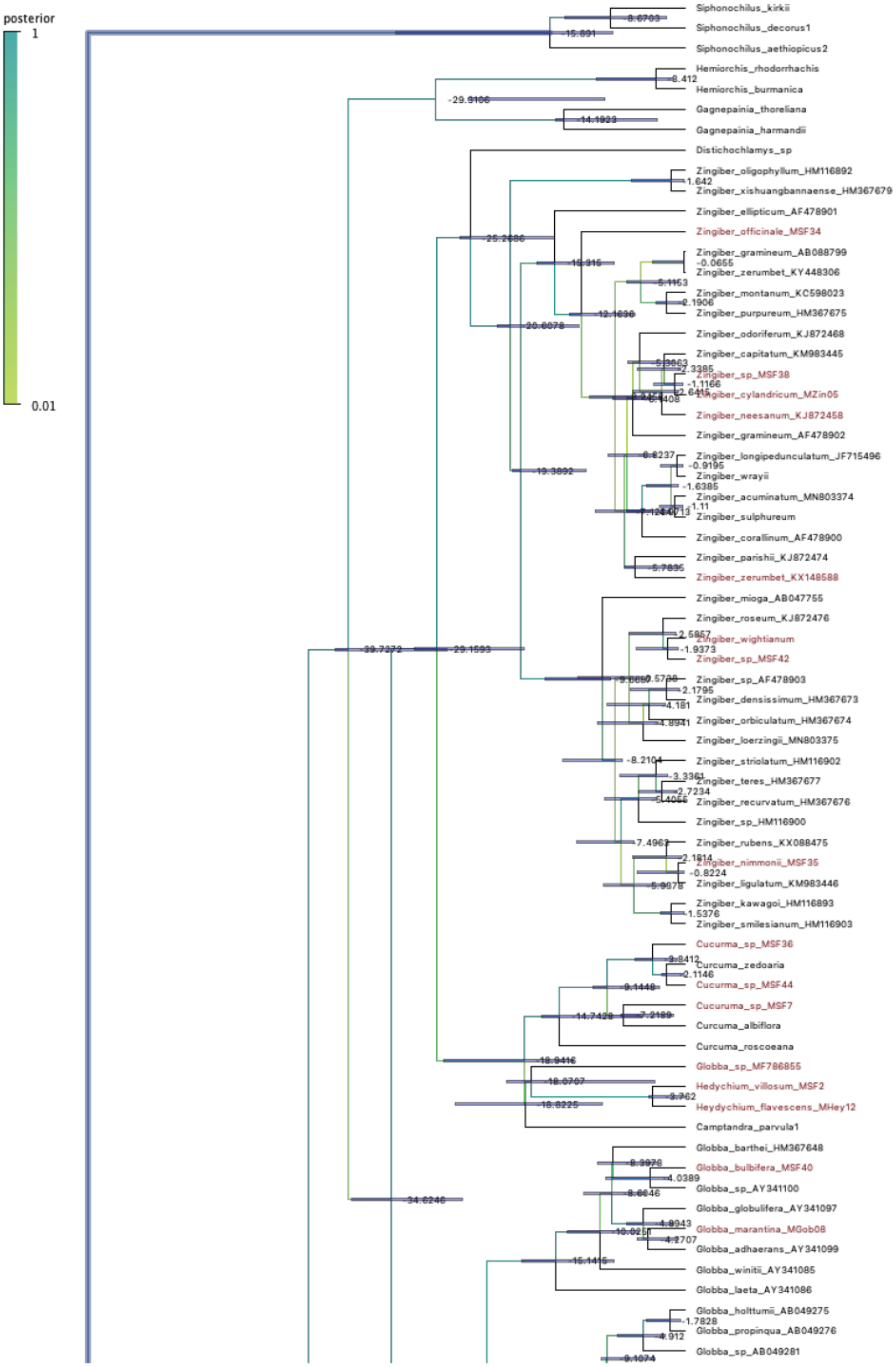
Amomum_sp3
99
Amomum_sp1
88
Amomum_acuminatum
0.007

Figure 3.31: Maximum Likelihood phylogeny for the family *Zingiberaceae*.

The maximum likelihood phylogeny was generated for 239 taxa using IQTREE for matK sequences. Samples in red indicate taxa found in the Western Ghats. Numbers on the nodes depict posterior probability values for the clades.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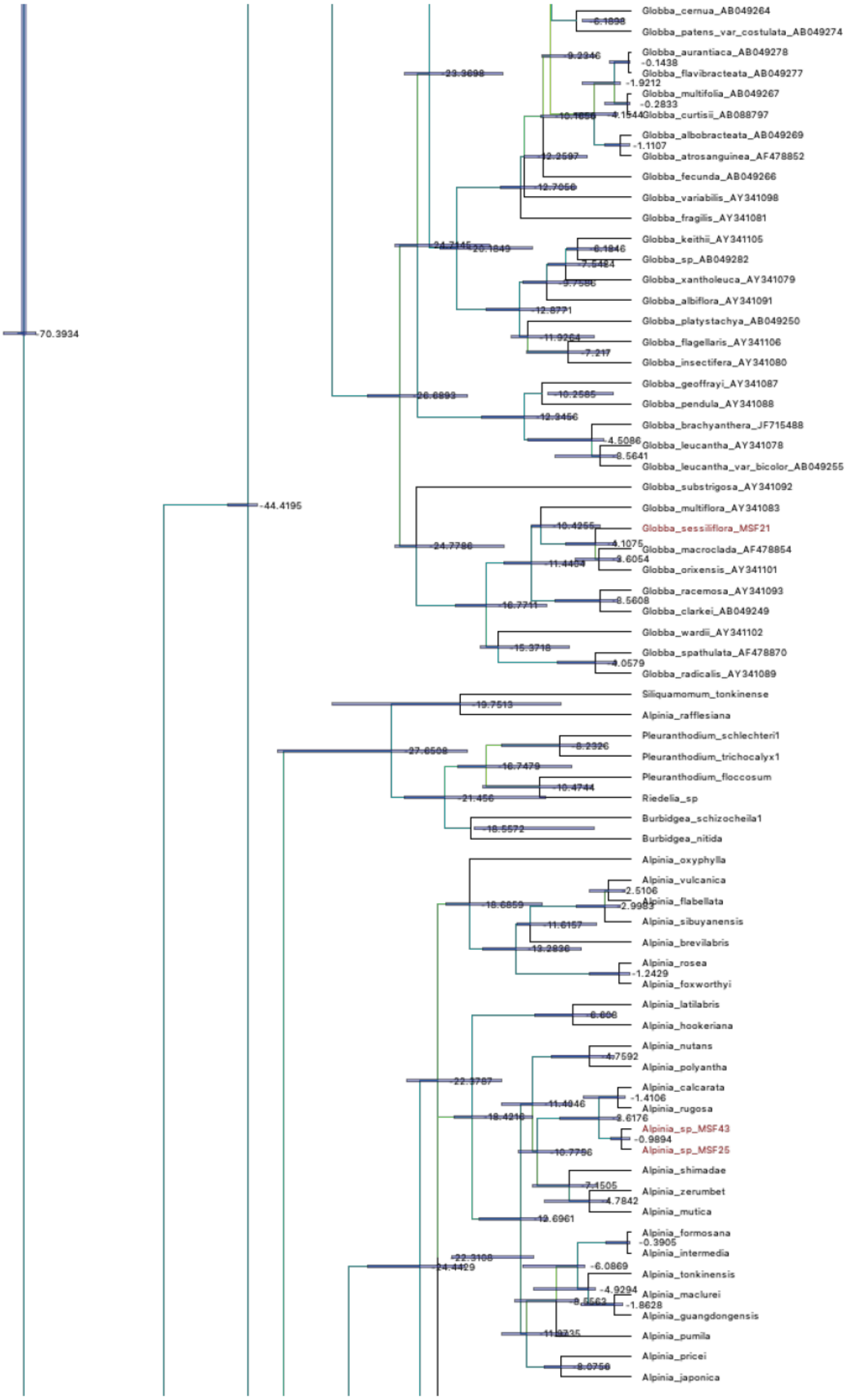
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Alpinia_sibuyanensis
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Alpinia_brevilabris
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Alpinia_rosea
1.2429
Alpinia_foxworthyi
Alpinia_latilabris
8.808
Alpinia_hookeriana
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11.4046
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Alpinia_sp_MSF25
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7.1505
Alpinia_zerumbet
4.7842
Alpinia_mutica
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Alpinia_formosana
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Alpinia_intermedia
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6.0869
Alpinia_tonkinensis
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Alpinia_maclurei
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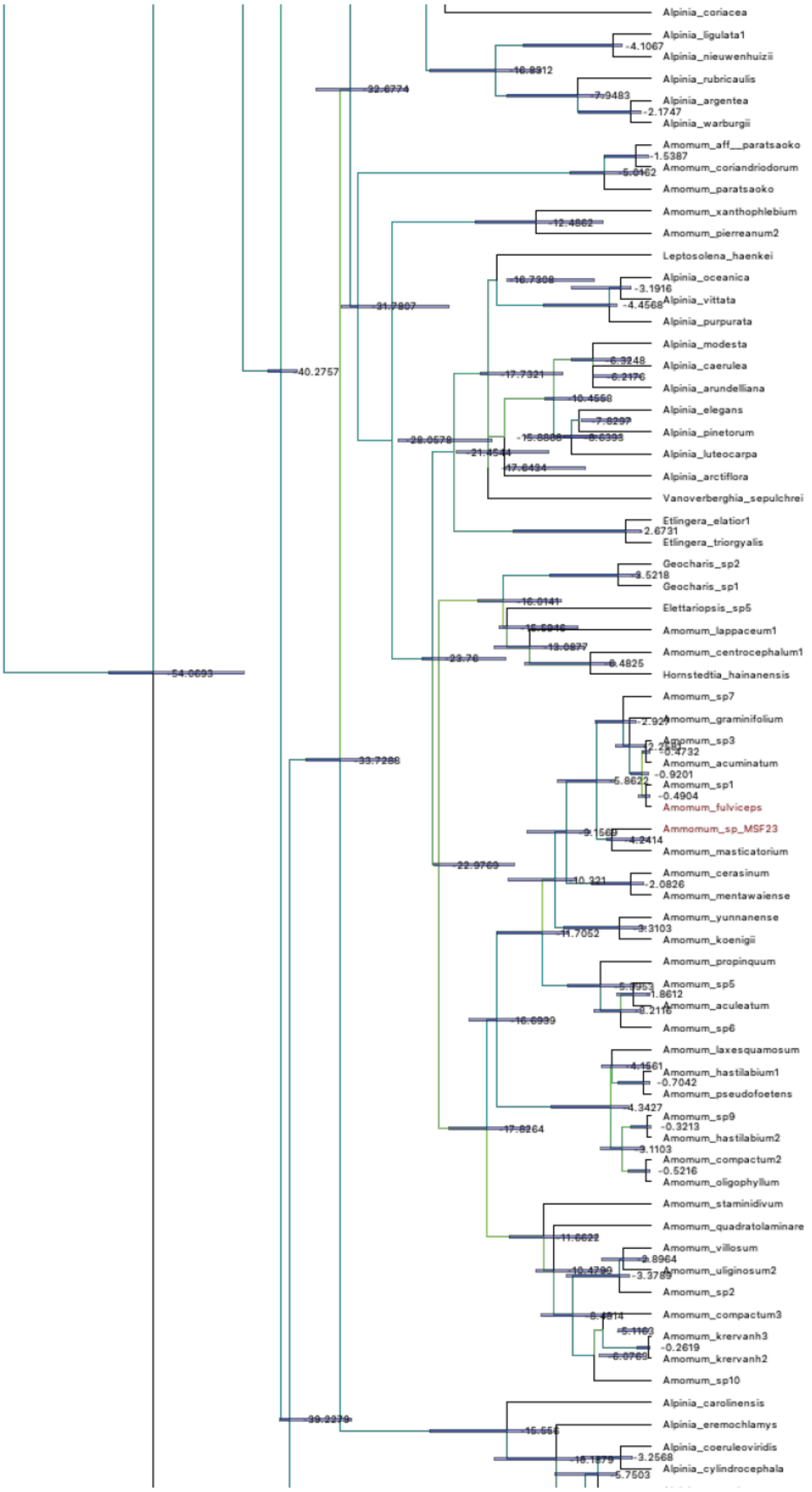
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Vanoverberghia_sepulchrei
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Amomum_staminidivum
Amomum_quadratolaminare
-11.6622
Amomum_villosum
-2.8964
-10.4799
-3.3789
Amomum_uliginosum2
Amomum_sp2
-8.4814
Amomum_compactum3
-5.1163
Amomum_krervanh3
-0.2619
-6.0769
Amomum_krervanh2
Amomum_sp10
Alpinia_carolinensis
Alpinia_eremochlamys
-39.2279
-15.556
Alpinia_coeruleoviridis
-18.1879
-3.2568
Alpinia_cylindrocephala
-5.7503

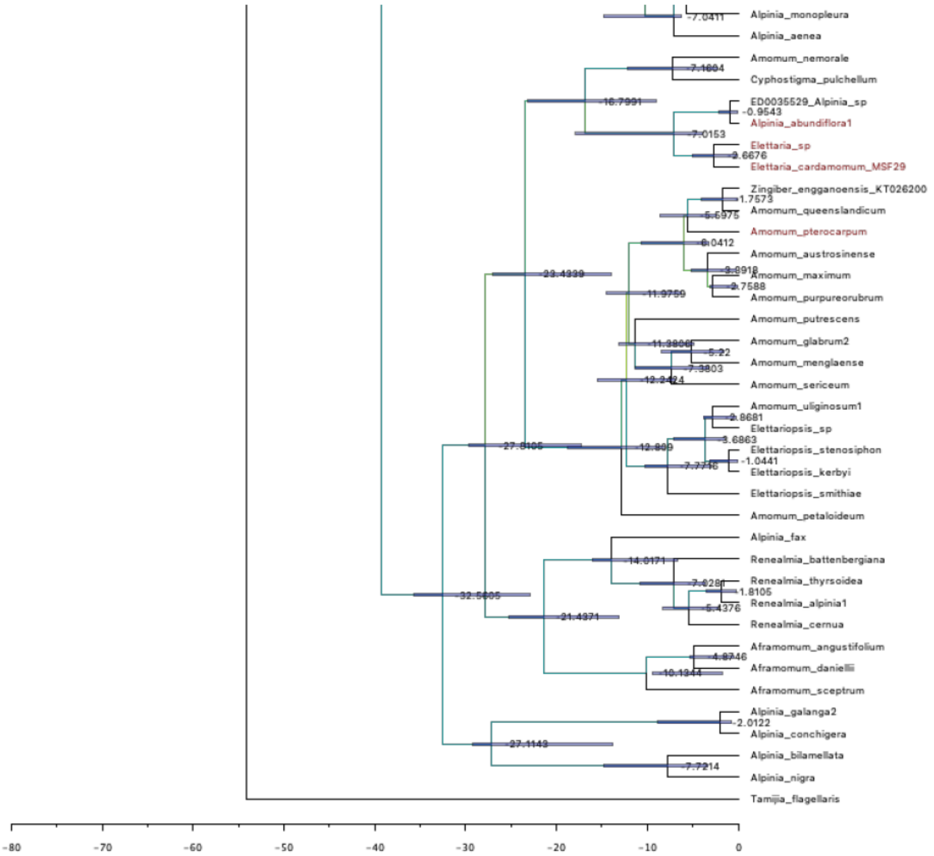
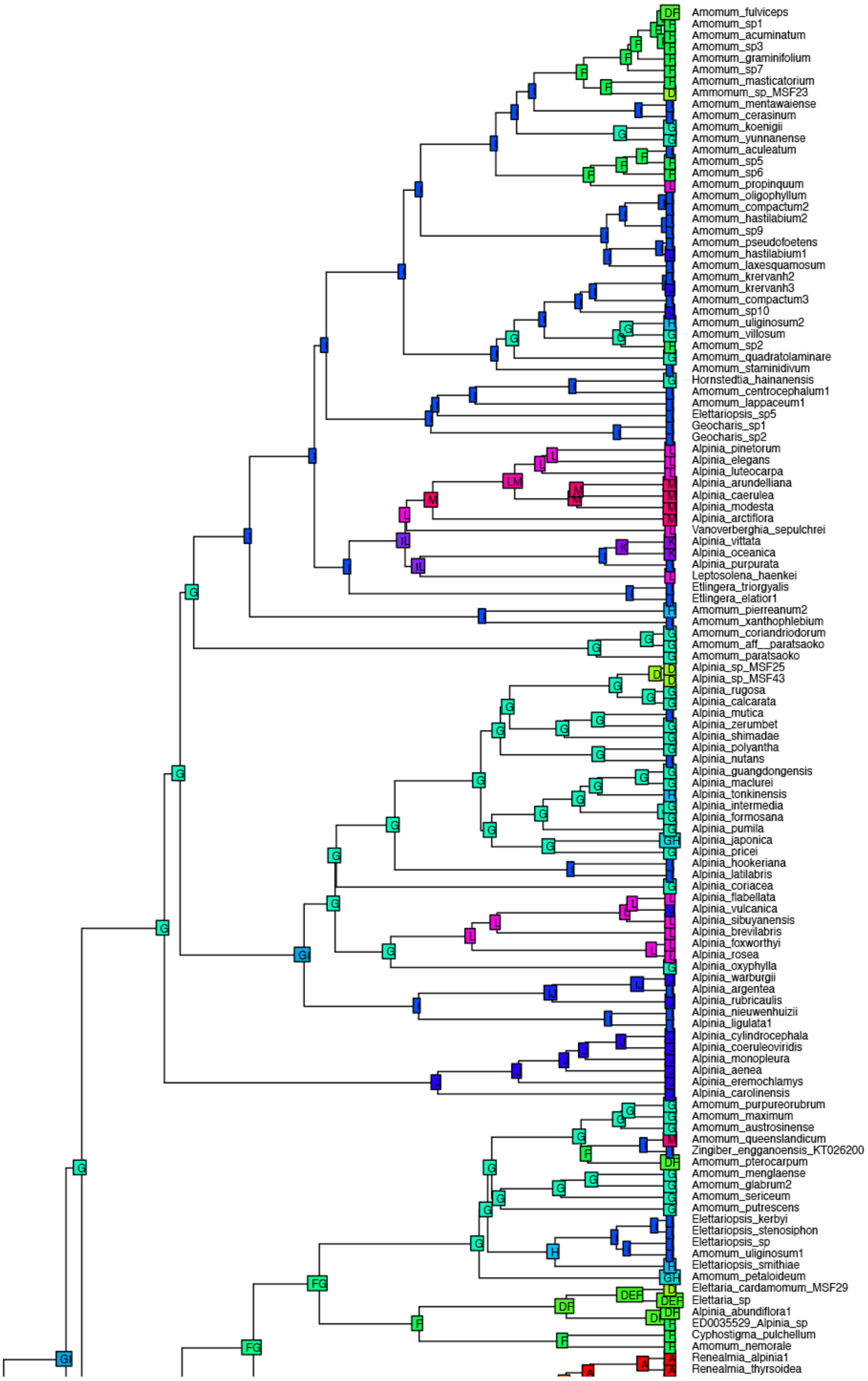


Figure 3.32: Time calibrated phylogeny of the family *Zingiberaceae* for 238 taxa.

Samples in red depict taxa endemic or native to the Western Ghats. The numbers on the nodes indicate mean ages with the node bars depicting 95% height HPD. Branch colours depict posterior probability of the clades with green being the lowest value and blue the highest.


Amomum_fulviceps
Amomum_sp1
Amomum_acuminatum
Amomum_sp3
Amomum_graminifolium
Amomum_sp7
Amomum_masticatorium
Ammomum_sp_MSF23
Amomum_mentawaiense
Amomum_cerasinum
Amomum_koenigii
Amomum_yunnanense
Amomum_aculeatum
Amomum_sp5
Amomum_sp6
Amomum_propinquum
Amomum_oligophyllum
Amomum_compactum2
Amomum_hastilabium2
Amomum_sp9
Amomum_pseudofoetens
Amomum_hastilabium1
Amomum_laxesquamosum
Amomum_krervanh2
Amomum_krervanh3
Amomum_compactum3
Amomum_sp10
Amomum_uliginosum2
Amomum_villosum
Amomum_sp2
Amomum_quadratolaminare
Amomum_staminidivum
Hornstedtia_hainanensis
Amomum_centrocephalum1
Amomum_lappaceum1
Elettariopsis_sp5
Geocharis_sp1
Geocharis_sp2
Alpinia_pinetorum
Alpinia_elegans
Alpinia_luteocarpa
Alpinia_arundelliana
Alpinia_caerulea
Alpinia_modesta
Alpinia_arctiflora
Vanoverberghia_sepulchrei
Alpinia_vittata
Alpinia_oceanica
Alpinia_purpurata
Leptosolena_haenkei
Etlingera_triorgyalis
Etlingera_elatior1
Amomum_pierreanum2
Amomum_xanthophlebium
Amomum_coriandriodorum
Amomum_aff__paratsaoko
Amomum_paratsaoko
Alpinia_sp_MSF25
Alpinia_sp_MSF43
Alpinia_rugosa
Alpinia_calcarata
Alpinia_mutica
Alpinia_zerumbet
Alpinia_shimadae
Alpinia_polyantha
Alpinia_nutans
Alpinia_guangdongensis
Alpinia_maclurei
Alpinia_tonkinensis
Alpinia_intermedia
Alpinia_formosana
Alpinia_pumila
Alpinia_japonica
Alpinia_pricei
Alpinia_hookeriana
Alpinia_latilabris
Alpinia_coriacea
Alpinia_flabellata
Alpinia_vulcanica
Alpinia_sibuyanensis
Alpinia_brevilabris
Alpinia_foxworthyi
Alpinia_rosea
Alpinia_oxyphylla
Alpinia_warburgii
Alpinia_argentea
Alpinia_rubricaulis
Alpinia_nieuwenhuizii
Alpinia_ligulata1
Alpinia_cylindrocephala
Alpinia_coeruleoviridis
Alpinia_monopleura
Alpinia_aenea
Alpinia_eremochlamys
Alpinia_carolinensis
Amomum_purpureorubrum
Amomum_maximum
Amomum_austrosinense
Amomum_queenslandicum
Zingiber_engganoensis_KT026200
Amomum_pterocarpum
Amomum_menglaense
Amomum_glabrum2
Amomum_sericeum
Amomum_putrescens
Elettariopsis_kerbyi
Elettariopsis_stenosiphon
Elettariopsis_sp
Amomum_uliginosum1
Elettariopsis_smithiae
Amomum_petaloideum
Elettaria_cardamomum_MSF29
Elettaria_sp
Alpinia_abundiflora1
ED0035529_Alpinia_sp
Cyphostigma_pulchellum
Amomum_nemorale
Renealmia_alpinia1
Renealmia_thyrsoidea

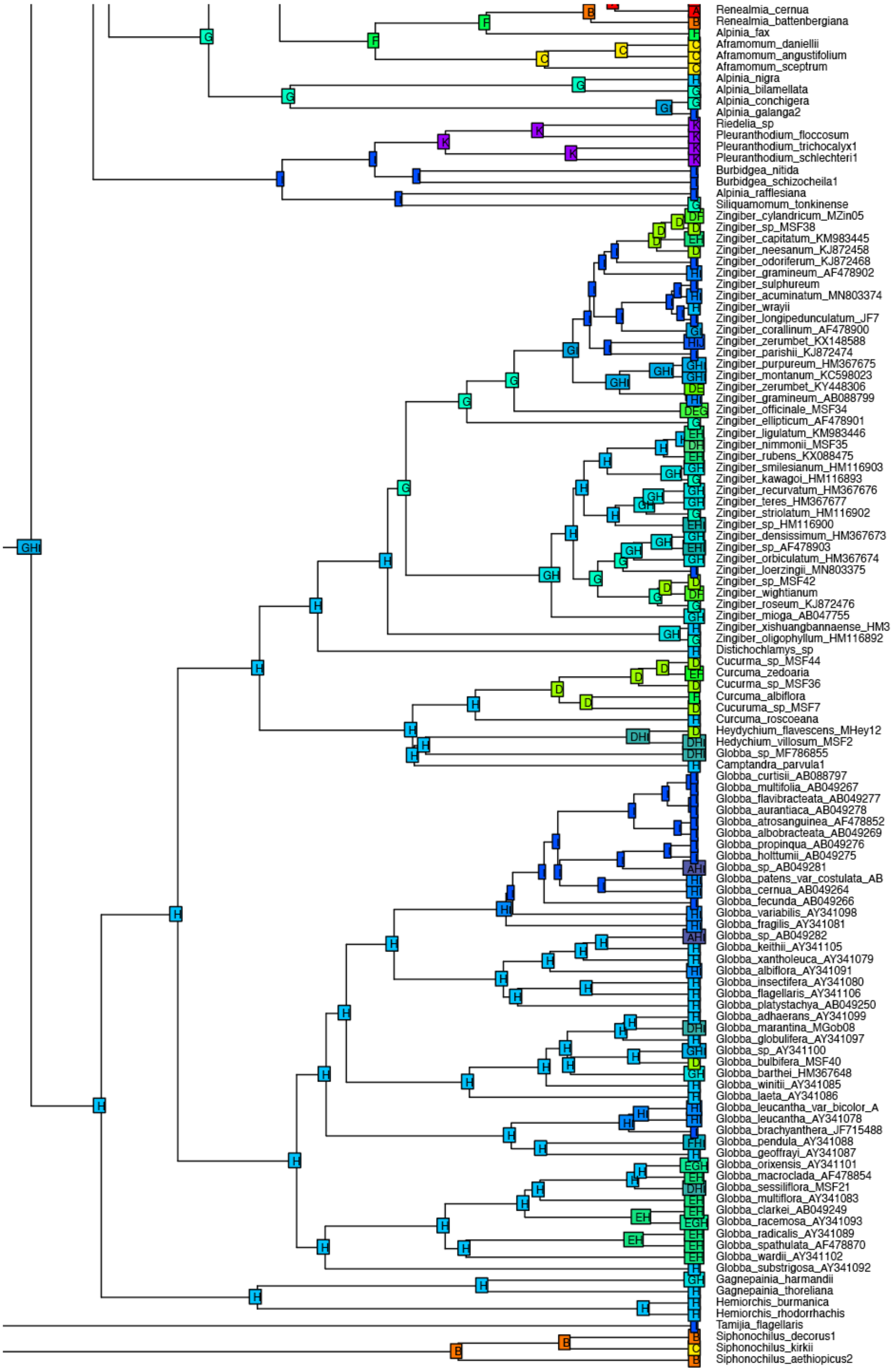


Figure 3.33: DEC+J ancestral area reconstruction for the family *Zingiberaceae*.

Geographic areas are coded as follows – A=America (Red), B=Africa (Orange), C=Madagascar (Yellow), D=Western Ghats (Light green), E=Himalayas (Green), F=Sri Lanka (Neon green), G=China (Turquoise), H=Continental Asia (Light blue), I=Sunda Shelf (Indigo). LnL value of -688.74. Clades listed in Table 3.7.

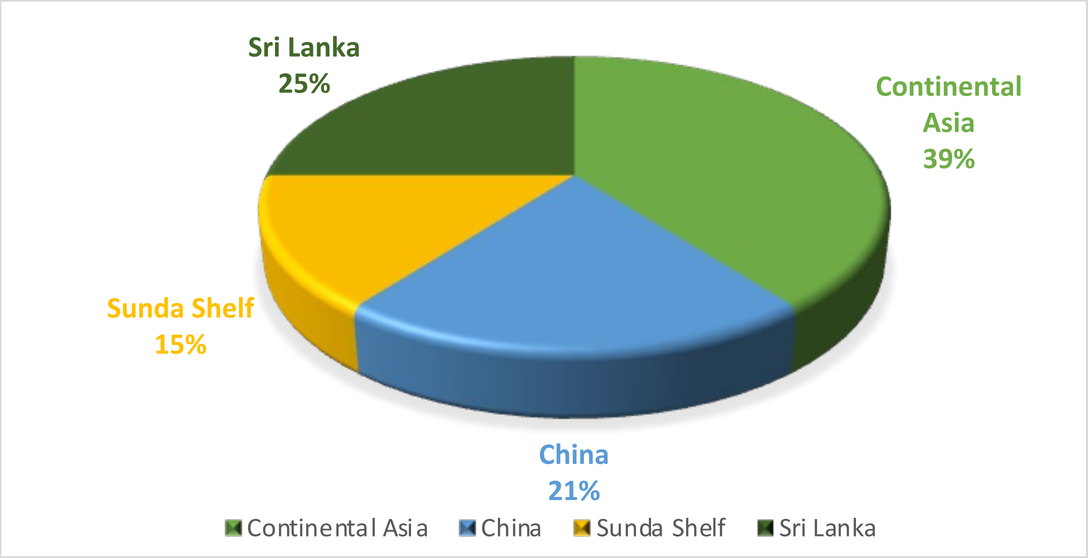


Figure 3.34: Pie chart depicting the geographic areas of origins for the Western Ghats clades of *Zingiberaceae*

Clade	**Taxa in clade**	**Minimum age (mya)**	**Area code**
Zingiberaceae I	*Globba sessiliflora MSF21*	4.11	H
Zingiberaceae II	*Globba bulbifera*	4.04	H
Zingiberaceae III	*Globba marantina MGob08*	4.27	H
Zingiberaceae IV	*Hedychium flavescens MHey12, Hedychium villosum MSF2, Globba sp MF786855*	18.07	H
Zingiberaceae V	*Curcuma sp MSF7, Curcuma sp MSF36, Curcuma sp MSF44*	14.74	H
Zingiberaceae VI	*Zingiber sp MSF42, Zingiber wightianum*	2.59	G
Zingiberaceae VII	*Zingiber nimmonii*	0.82	H
Zingiberaceae VIII	*Zingiber officinale MSF34*	12.16	G
Zingiberaceae IX	*Zingiber zerumbet*	5.12	GHI
Zingiberaceae X	*Zingiber neesanum,*	5.31	I
Zingiberaceae XI	*Zingiber cylindricum MZin05, Zingiber sp MSF38*	5.31	I
Zingiberaceae XII	*Alpinia abundiflora1, Elettaria sp, Elettaria cardamomum MS29*	16.8	F
Zingiberaceae XIII	*Amomum pterocarpum*	5.6	F
Zingiberaceae XIV	*Alpinia sp MSF43, Alpinia sp MSF25*	3.62	G
Zingiberaceae XV	*Amomum sp MSF23*	4.24	F
Zingiberaceae XVI	*Amomum fulviceps*	0.47	F

Table 3.7: *Zingiberaceae* table showing clade number, taxa found in each clade, their minimum age, and geographic origin.

3.4 Data Synthesis

3.4.1 Age of arrival

The flora of the Western Ghats as depicted by the Age of Disjunction graph (Figure 3.35) appears to be geologically young, with the vast majority of the clades and species in this study having arrived between the Oligocene and the Pliocene. This scatter plot represents dispersal events for thirteen angiosperm families, with 66 clades from this study and 9 clades from other published studies of angiosperms in the region (Bajpe et al., 2023; Liu et al., 2018; Neupane et al., 2017; Puri et al., 2016; Sen et al., 2019; Tsai et al., 2020; Yuan et al., 2005). Movement to the Western Ghats appears to have been from several geographic regions (Figure 3.36). Large parts of the flora have arrived to the Ghats from the regions of Continental Asia and the Sunda Shelf, with some from Sri Lanka and China. The flora also has dispersals from Africa and Madagascar, with minor dispersal from Australia, the Himalayas and America. The geographic origins are not constant amongst the families, each family arrived to the Ghats from different areas.

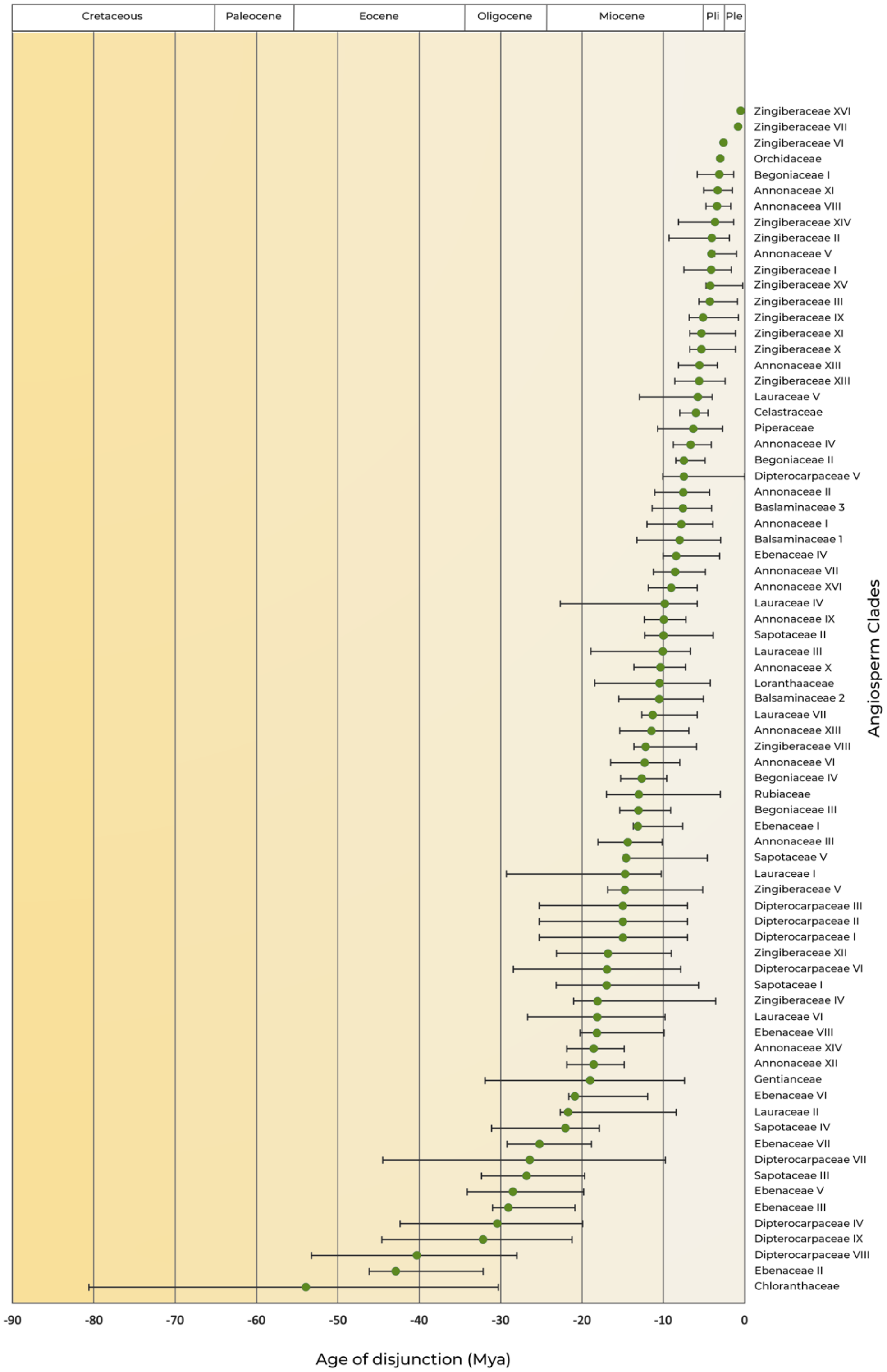


Figure 3.35: Scatter plot depicting the minimum ages of 75 Western Ghats clades.

The clades are ordered youngest to oldest going down the y-axis. The error bars depict the 95% HPD ages of the clades. 66 clades were added from this study and the remaining 9 are from other published studies within the region.

3.4.2 Geographic origin of clades

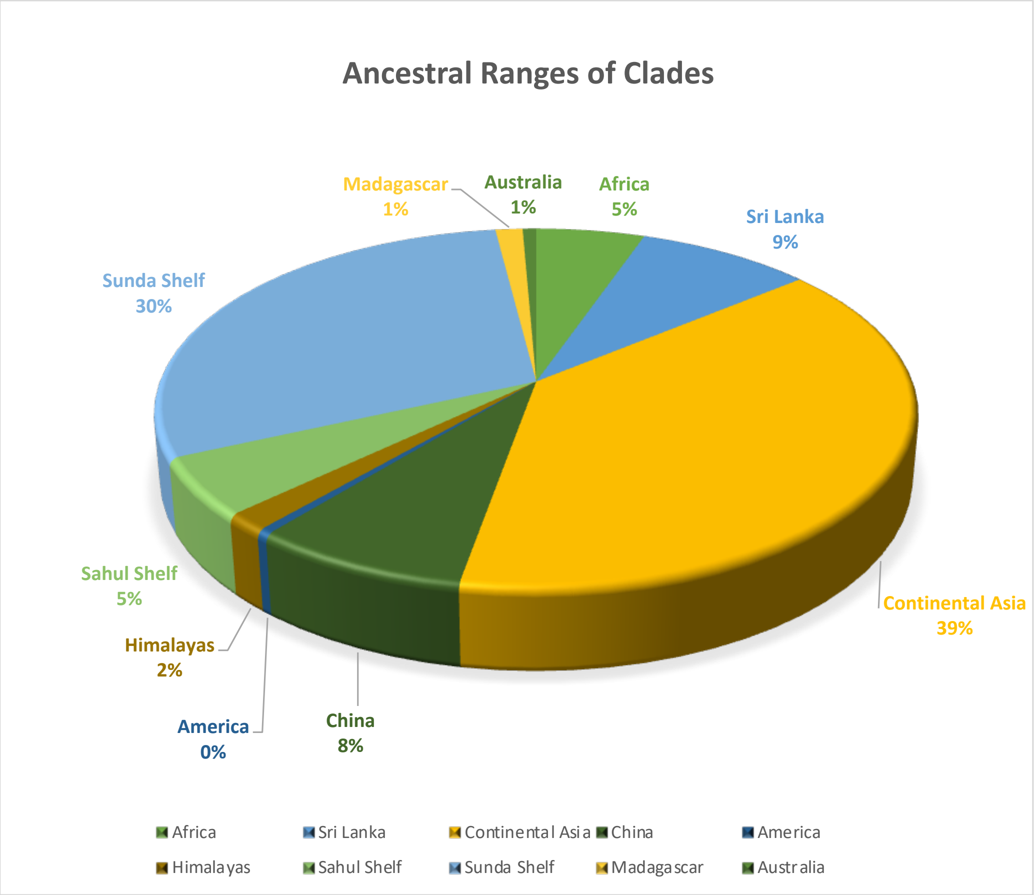


Figure 3.36: Pie graph depicting the ancestral ranges of 15 angiosperm families into the Western Ghats.

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Chapter 4

Discussion

Exploring the floristic history of the Western Ghats

Madapura Range, Somwarpet, Kodagu District, Karnataka, September 2022.

List of Figures

There is an unequal distribution of plant biodiversity in the world. This diversity is largely associated with latitude, found to be highest along the equator, and also associated with mountainous regions (Gaston and Blackburn, 1996). The geological ages and geographic origins of species found within these hotspots are vital to our understanding of this variation. To date most studies have focused on geologically younger mountain systems, hence, to address this bias this study focuses on a much older range – the Western Ghats. This fragmented yet magnificent range was formed when India separated from Gondwana c.150 million years ago (Briggs, 2003). The Ghats currently lie entirely within the tropical belt and are extremely rich in plant diversity, making them an excellent study area for the presence of Gondwanan relics as well as recently accumulated species. The combination of climate epochs, latitudinal gradients, and other geological events traversed by the Indian subcontinent over c.100 million years makes for a remarkable story. One that is addressed in this study from the perspective of flowering plants.

This study analysed the age and geographic origin of 75 arrivals of flowering plants native or endemic to the Western Ghats. These arrivals are comprised of newly gathered data for 66 clades belonging to the angiosperm families *Annonaceae*, *Begoniaceae*, *Chloranthaceae*, *Dipterocarpaceae*, *Ebenaceae*, *Lauraceae*, *Sapotaceae*, and *Zingiberaceae*, and nine additional clades in the families *Balsaminaceae*, *Celastraceae*, *Gentianaceae*, *Loranthaceae*, *Orchidaceae*, *Rubiaceae*, and *Piperaceae* from other published studies within the region (Bajpe et al., 2023; Liu et al., 2018; Neupane et al., 2017; Puri et al., 2016; Sen et al., 2019; Tsai et al., 2020; Yuan et al., 2005). Of the 75 clades addressed in this study, most arrivals were seen in the Miocene (49 clades) and the Pliocene (15 clades). The geographic origins of these clades largely favour the areas of Continental Asia and the Sunda Shelf, with other regions such as Africa and Madagascar playing a smaller role. There are two theories with respect to how these clades may have arrived to the Western Ghats – (1) Vicariance – The subcontinent of India as it journeyed towards the Eurasian plate became a raft for Gondwanan species, both flora and fauna (2) Dispersal/Migration, which can be divided into two scenarios – (i) Contact with the Sunda Shelf and Myanmar prior to collision, (ii) Post collision. These two major theories are addressed by following the Indian subcontinent's voyage through the geological ages.

4.1 Vicariance

4.1.1 The Indian Subcontinent as a raft

Late Jurassic – Paleocene (155 – 56 million years ago)

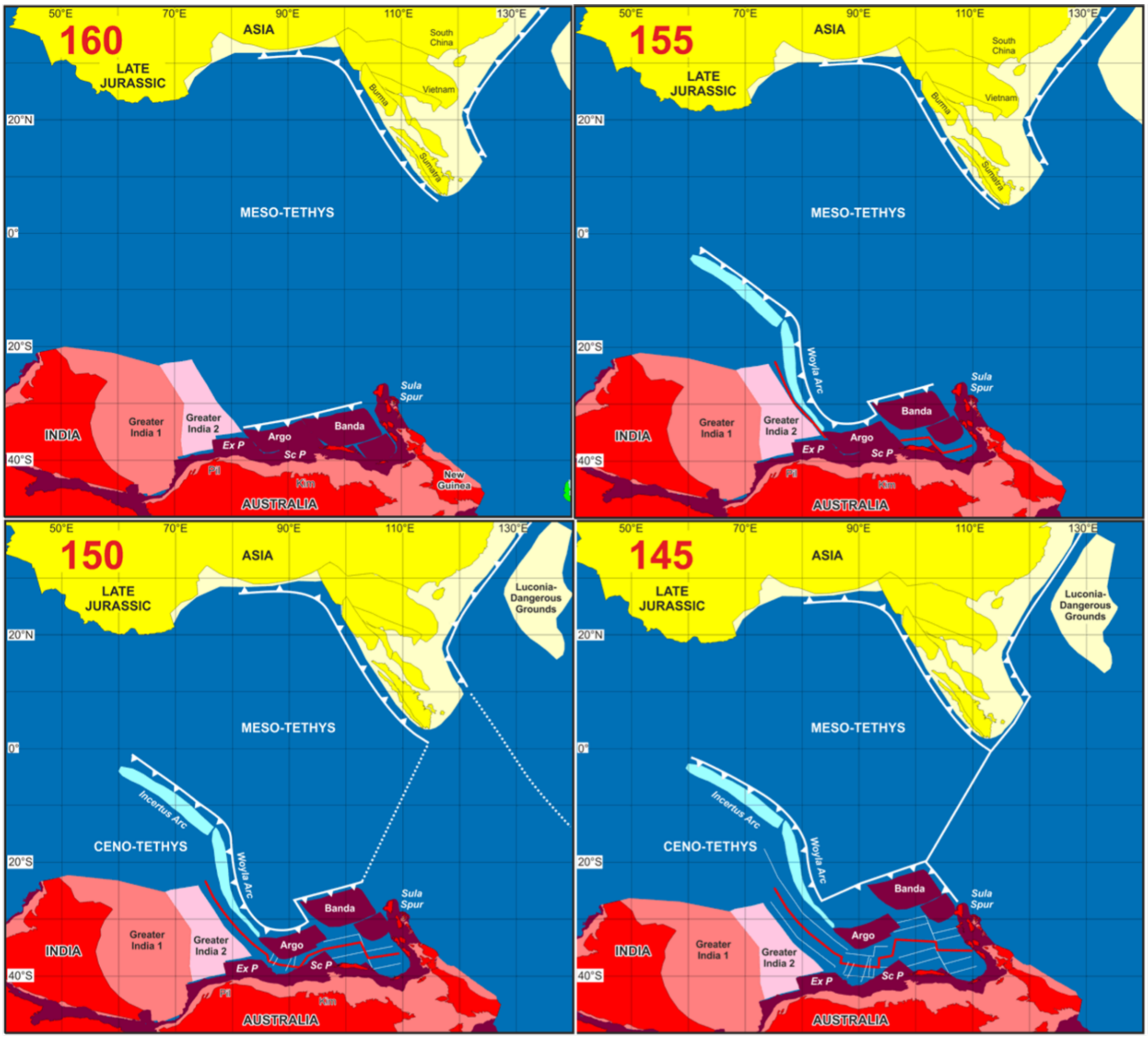

Figure 4.1: Plate tectonics in the Late Jurassic period (Hall, 2012).

During the existence of Gondwana (Late Jurassic), the region which was to form the Indian subcontinent was placed with Africa and Madagascar in the West, Sri Lanka in the Southeast, and Antarctica and Australia in the East (Figure 4.1). The subcontinent sat in the Southern Hemisphere at a latitude of 30° S (Ghosh et al., 2018; Hall, 2012), almost perpendicular to its current position. In terms of the world today, the Northern states of the Western Ghats – Gujarat and Maharashtra were adjacent to Somalia whilst the Central and Southern states of the Ghats – Goa, Karnataka, and Kerala were adjacent to Madagascar. In the Late Jurassic period India, Madagascar and the Seychelles separated from the African landmass (Bossuyt, 2004; Briggs, 2003). By the Early Cretaceous the Indian plate had separated from Antarctica and Australia (Chatterjee et al., 2013) and had begun its upwards journey towards the Eurasian plate.

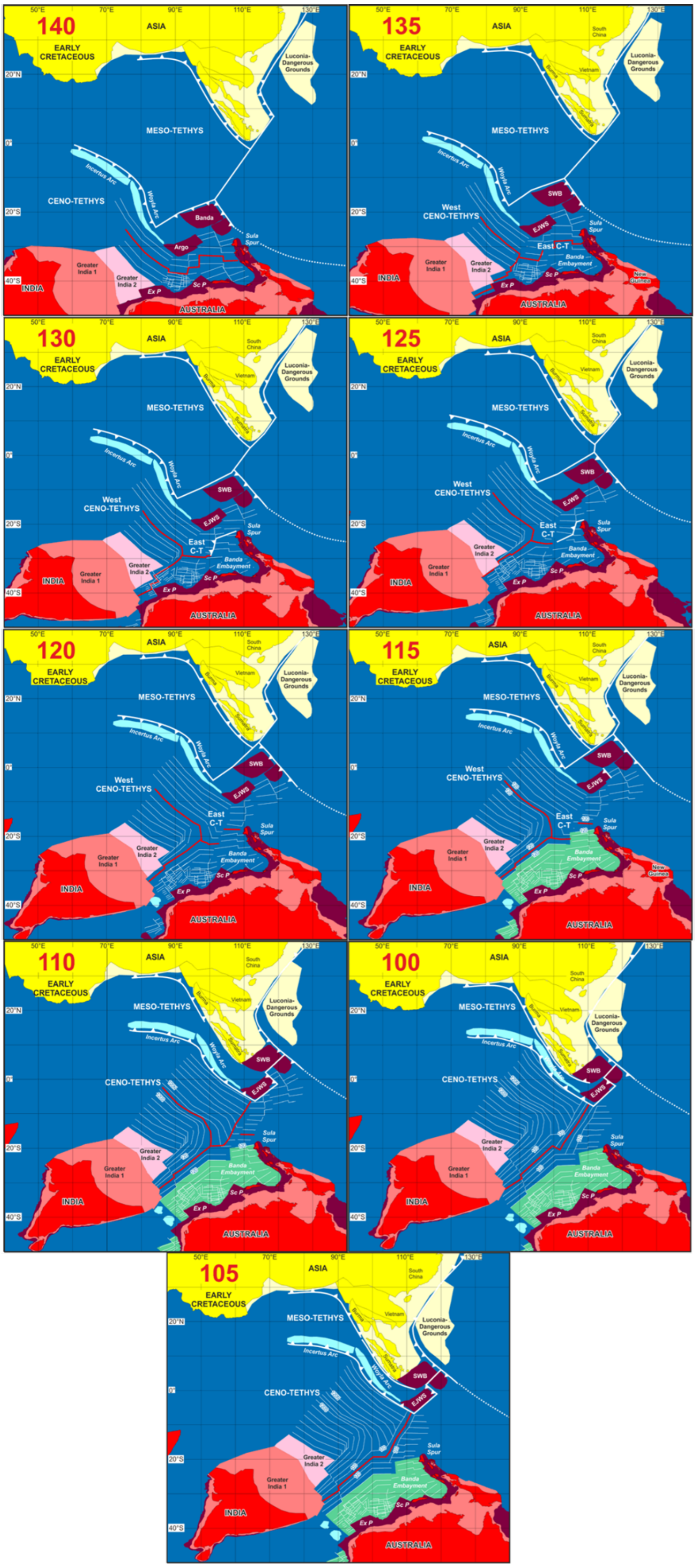

Figure 4.2: The Indian plate in the Early Cretaceous period (Hall, 2012)

In the Early Cretaceous both sea surface temperatures and levels were high (Anderson et al., 1999; Littler et al., 2011). This changed in the mid Cretaceous where the temperatures became warm and tropical, perfect for the rise of flowering plants (Anderson et al., 1999; Pearson. et al., 2001; Zhao et al., 2022). Fossils of angiosperms belonging to the orders Sapindales and Malvales have been found in the Deccan Traps dating back to the Cretaceous period (Bhatia et al., 2021; Morley, 2018). At this time the subcontinent of India was still attached to the landmasses of Madagascar and the Seychelles (Figure 4.2). Separation from the island of Madagascar occurred between 96-84 mya as a result of the Marion hotspot plume (Briggs, 2003). No clades have been found arriving to the Western Ghats from the Early Cretaceous in this study, yet the subcontinent must have had elements of a vicariant flora, as amber carrying angiosperms has been found in Myanmar dating back to the Early Cretaceous, indicating the possibility of vicariance having occurred on the West Burma Terrane (BT) (Huang et al., 2021; Poinar, 2019). The BT block, today a part of Myanmar, is a landmass that was once part of Northern Gondwana (Morley et al., 2021).

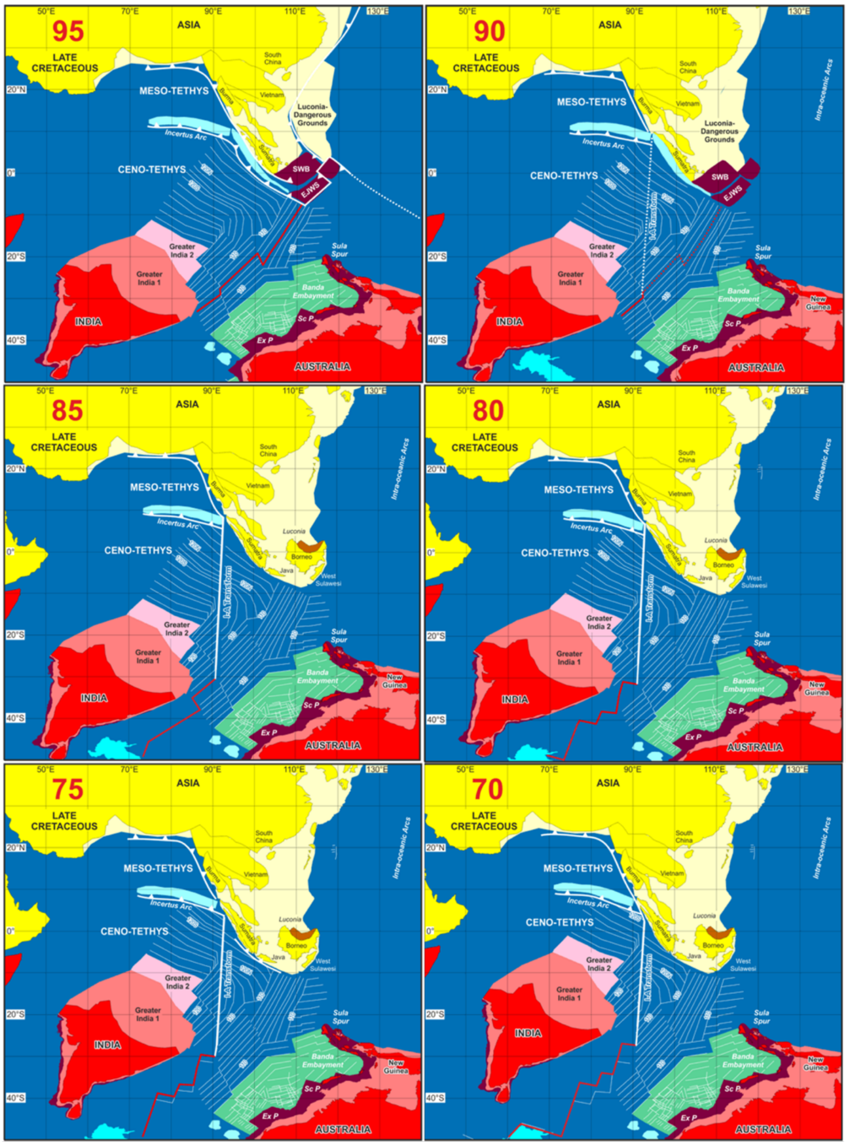

Figure 4.3: Movement of the Indian plate across the Tethys Sea in the Late Cretaceous period (Hall, 2012).

As India moved up through the latitudes it rotated anti-clockwise (Gnos *et al.*, 1997) (Figure 4.3). Separation from the Seychelles occurred before the Deccan volcanic event at the Cretaceous-Paleogene boundary (Chatterjee et al., 2013). It has been conjectured that the rifting between India and the Seychelles aggravated the intensity of volcanic activity (Chatterjee et al., 2013). The result of this volcanic activity is the widespread basalt flood plain – the Deccan Traps (Joshi and Karanth, 2013) spanning approximately 500,000 km^2 (Bhatia et al., 2021). The Deccan traps cover most of northern peninsular India, and some parts of central and southern India extending out into the Arabian Sea (Bhatia et al., 2021; Chatterjee and Rudra, 1996). There exists evidence that at the same time the Deccan volcanic event occurred multiple asteroids collided with Earth (Burnham and Morley, 2000; Chatterjee and Rudra, 1996).

In roughly the last 10 million years of the Cretaceous period, global climate went through four extreme changes (Mateo et al., 2017), with tropical temperatures in the mid-Cretaceous (Pearson. et al., 2001) followed by cycles of cooling and heating, with the final heating event of that epoch occurring at the cusp of the KT Boundary (Mateo et al., 2017). The end of the Cretaceous and the beginning of the Paleocene saw severe mass extinctions globally (Keller, 2008; Mateo et al., 2017) likely driven by the severe volcanism, meteor collisions, and rising sea surface temperatures of the time.

It has been found that during the early stages of separation from Gondwana, the flora of India resembled that of Australia (Burnham and Morley, 2000). This flora became more like that of Africa as it travelled up in the latitudes towards the equator (Burnham and Morley, 2000). In the Origin and Evolution of Tropical Rainforests, Morley states that "the Indian Plate bore a flora with three distinct components: an ancient autochtonous gondwanic component, carried from Gondwana, and consisting principally of gymnosperms and pteridophytes, possibly with a few angiosperms; an allochtonous component from Africa, consisting of megathermal angiosperm elements; and a diverse endemic component which evolved as India drifted across many climatic zones.", indicating that the presence of wet forests on the Indian subcontinent in the mid Cretaceous was very likely (Burnham and Morley, 2000). The extant families of *Chloranthaceae* and *Winteraceae*, are said to have been important components of tropical flora at this time (Burnham and Morley, 2000).

The extended isolation period of the Indian landmass would imply that Gondwanan relics had time to evolve to become India's own brand of floristic endemicity (Burnham and Morley, 2000; Chatterjee et al., 2013). In fact, perfectly preserved fossils have been found in the Deccan Traps of various taxa including those of *Anacardiaceae, Myrtaceae, and Moraceae* (c.70 to 55 mya) (Bhatia et al., 2021; Rajasri et al., 2020; Wheeler et al., 2017), as well as the oldest known grape (*Vitaceae*, c.66 myr) fossil (Manchester et al., 2013). Although the lava from the Deccan volcanic event covered a large portion of northern peninsular India, the Southern Western Ghats were potentially a biological safe house for some Gondwanan relics, as demonstrated by the centipede genus *Digitipes* (Joshi and Karanth, 2013). If this were the case for plants, we should see far more clades with Africa or Madagascar as ancestral ranges. However, the mass extinctions and climatic events of Cretaceous-Paleocene boundary (Karanth, 2006) seem to have disproportionately affected the flora, which is why there are no Gondwanan relics amongst the fifteen angiosperm families studied here. This study finds no direct evidence for Gondwanan vicariance as an explanation for the origin of the extant angiosperm diversity in the Western Ghats.

4.2 Dispersal

4.2.1 Possible contact with Sunda and Continental Asia

Paleocene (66 – 56 million years ago)

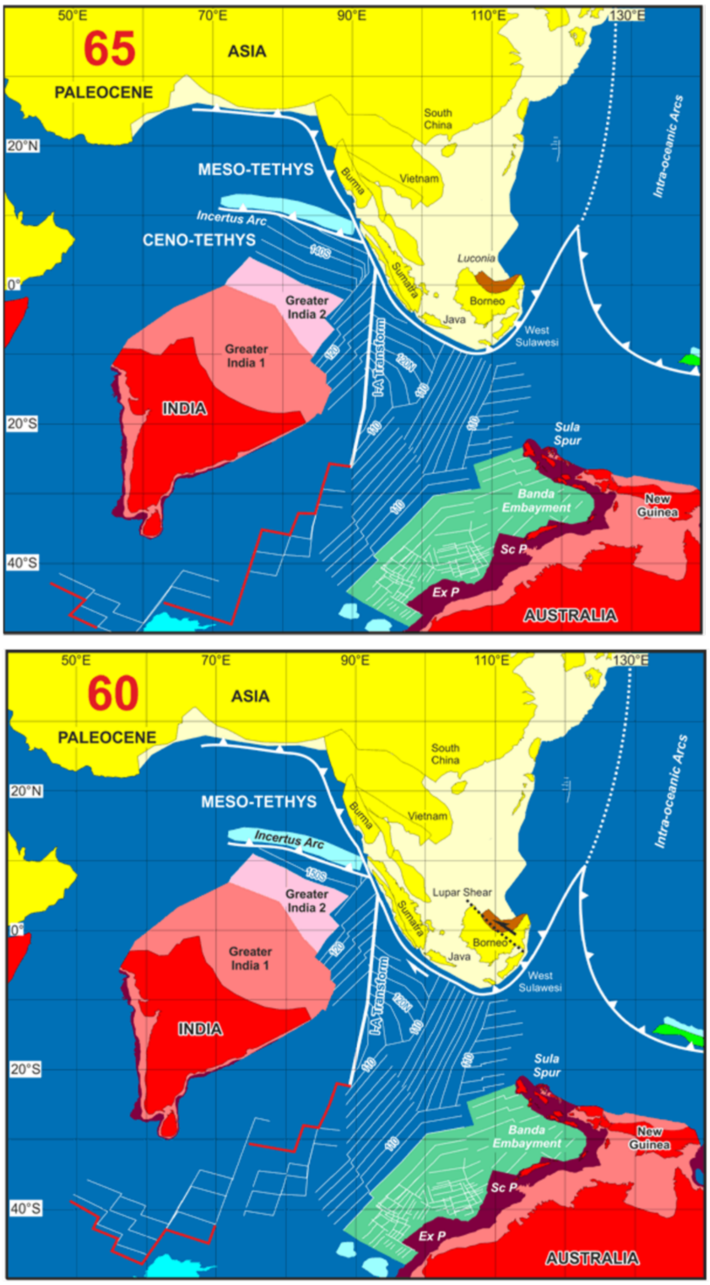

Figure 4.4: The movement of the Indian plate across the Tethys Sea during the Paleocene (Hall, 2012).

The Paleocene, witnessed high temperatures referred to as the Paleocene-Eocene Thermal Maximum (PETM) (Huang et al., 2016; McInerney and Wing, 2011). At this point in time most of the Indian subcontinent remained in the Southern Hemisphere, while Greater India had just crossed the equator (Hall, 2012) (Figure 4.4). Geologists have proposed that contact with Asia occurred much before the uplift of the Himalayas, possibly as early as the Late Paleocene via contact with Sumatra and then Myanmar by the far north of the plate as it rotated and slotted into track for its imminent collision with Tibet (Ali and Aitchison, 2008). Theoretically this would facilitate floristic exchange between India, Continental Asia and the Sunda Shelf, however this study found no signal of this in the extant flora of the regions concerned. It is possible that climatic factors may have worked against floristic exchange at this time, or that the distances were greater than geological theories suggest. However, it is also possible that exchange did occur and no evidence exists of it in the extant flora as a consequence of it being over-written by further dispersal and extinction events.

4.2.2 Post Collision

Eocene (56 – 33.9 million years ago)

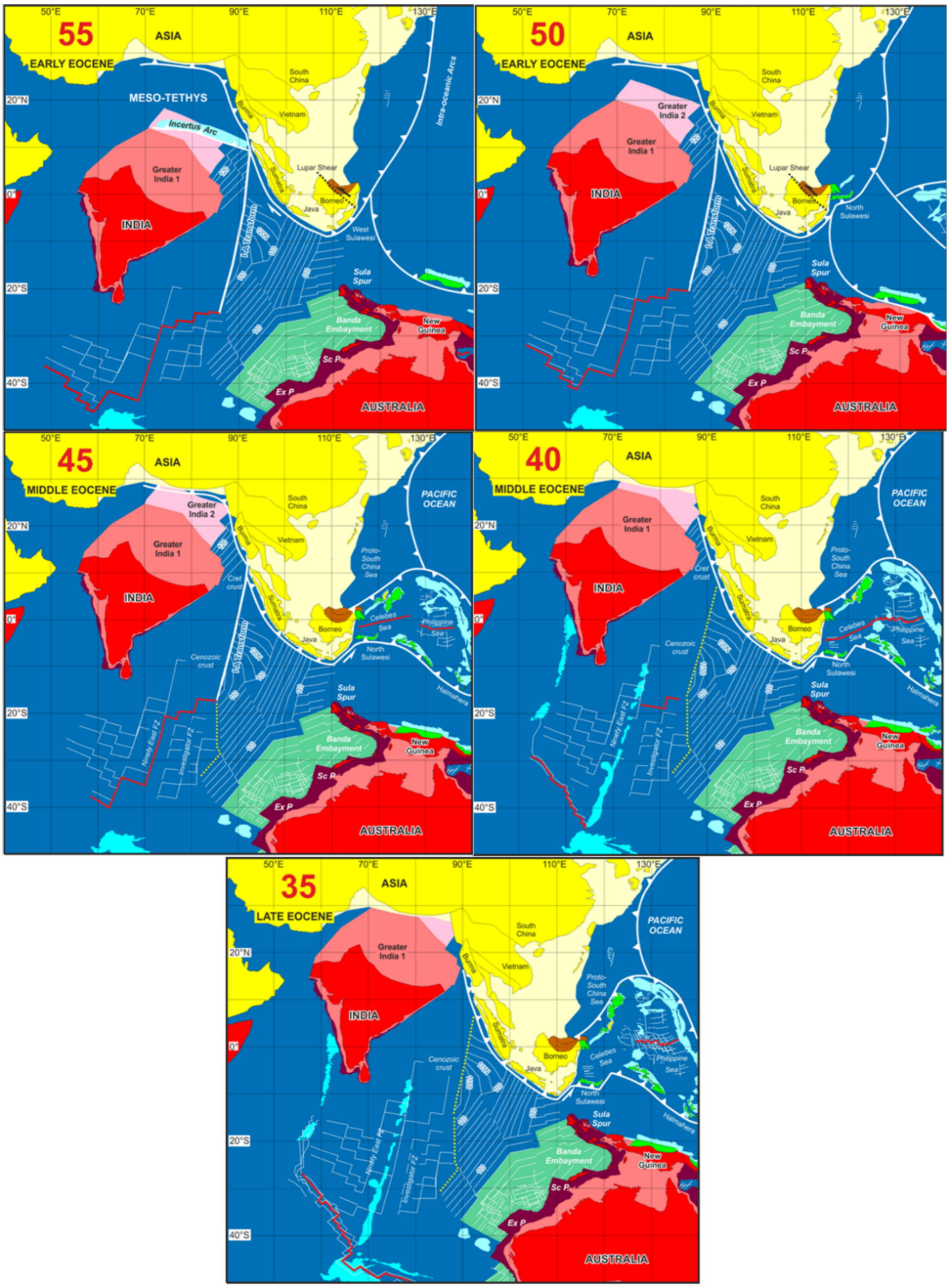

Figure 4.5: The movement and collision of the Indian plate with the Eurasian plate in the Eocene. Images taken from (Hall, 2012).

After the devastating mass extinctions and high sea surface temperatures witnessed in the Paleocene (Mateo et al., 2017), the Eocene saw the climate mellowing to warm and tropical temperatures (Pearson. et al., 2001; Pearson et al., 2007) perfect for a flourishing of the angiosperms. Fossil evidence has been found suggesting that the Western Ghats may have behaved as a refugia for wet tropical forests during the PETM (Prasad et al., 2009). The Indian subcontinent was now fully situated in the tropical/equatorial belt with Greater India in the Northern Hemisphere and peninsular India in the Southern Hemisphere (Burnham and Morley, 2000; Hall, 2012) (Figure 4.5). The plate subsequently collided with the Lhasa block near Tibet in the Eocene and thus began the uplift of the world's tallest mountain range – the Himalayas (Ali and Aitchison, 2008; Chatterjee et al., 2013), and because of it a land bridge between India and Continental Asia. Between c.54 mya and c.40 mya, the Ghats saw the arrival of three clades from three families – *Dipterocarpaceae*, *Ebenaceae* (*Diospyros*), and *Chloranthaceae*.

At c.54 myr the largely bird-dispersed tree family *Chloranthaceae* arrived to the Western Ghats during a single clade which showed a widespread geographic origin of China, Continental Asia, and the Sunda and Sahul Shelves. The arrival of the *Chloranthaceae* clade coincides with the time frame of collision of the Indian plate with Eurasia, giving potential for arrival of the family either via dispersal or migration. Previous work on this family showed a Cretaceous origin for *Chloranthaceae*, with a more recent origin for the crown group *Hedyosmum* in the Andes (Antonelli and Sanmartín, 2011). The study showed a family age that is congruent with the time frame of Gondwana, but as we see here in the molecular phylogenies, the age the extant flora is much younger.

A single clade of *Diospyros*, *Ebenaceae* (II) arrived to the Western Ghats c.43 mya from Continental Asia. One clade of the wind dispersed family *Dipterocarpaceae* (VIII) arrived c. 40 mya with a likely Sunda Shelf origin. There is fossil evidence of *Dipterocarpaceae* on the subcontinent from 52 mya, and a recent molecular study using DEC implemented in RASP showed evidence for a Gondwanan vicariant origin for the family (Sanil et al. 2002), with an area of origin comprising of India, Sri Lanka, Madagascar, and the Seychelles. Our study which was based on the same data with the addition of one sample from the Ghats, showed similar results with respect to an earlier role for diversification on the Sunda Shelf, but did not find a signal of deep vicariance. However, both studies show frequent interchange between India and Southeast Asia beginning ca. 30 mya. The difference in reconstruction at the base of the tree could be due to two factors– (i) a different method of distribution scoring – the dataset here considered the Western Ghats and Sri Lanka as unique floristic entities and (ii) a different biogeographic model – our study employed the DEC+J model. Both factors may work against detecting an already weak and overwritten signal of vicariance.

Dispersal in the Eocene was not one sided, with floral exchange likely occurring between India and Asia during India's journey towards the Asian plate and upon collision (Klaus et al., 2016; Morley, 2018). It has been theorised that the Indian flora had become fairly aggressive as the subcontinent travelled northeast, and this enabled some of its elements to rise to dominance in the rainforests of Continental and Southeast Asia, for example the families *Dipterocarpaceae*, *Malvaceae,* and *Podocarpaceae* (Morley, 2018, 2003; Sanil et al., 2022). The exchange between the rest of Asia and India occurred via dispersal and fossils dating back to the Eocene have been found on the subcontinent for the angiosperm families *Dipterocarpaceae, Ebenaceae, Sapotaceae, and Lauraceae* (Bhatia et al., 2021; Morley, 2018; Rust et al., 2010). The collision of the Indian plate is also said to be responsible for shaping the flora of Myanmar (Huang et al., 2021).

Oligocene (33.9 – 23.03 million years ago)

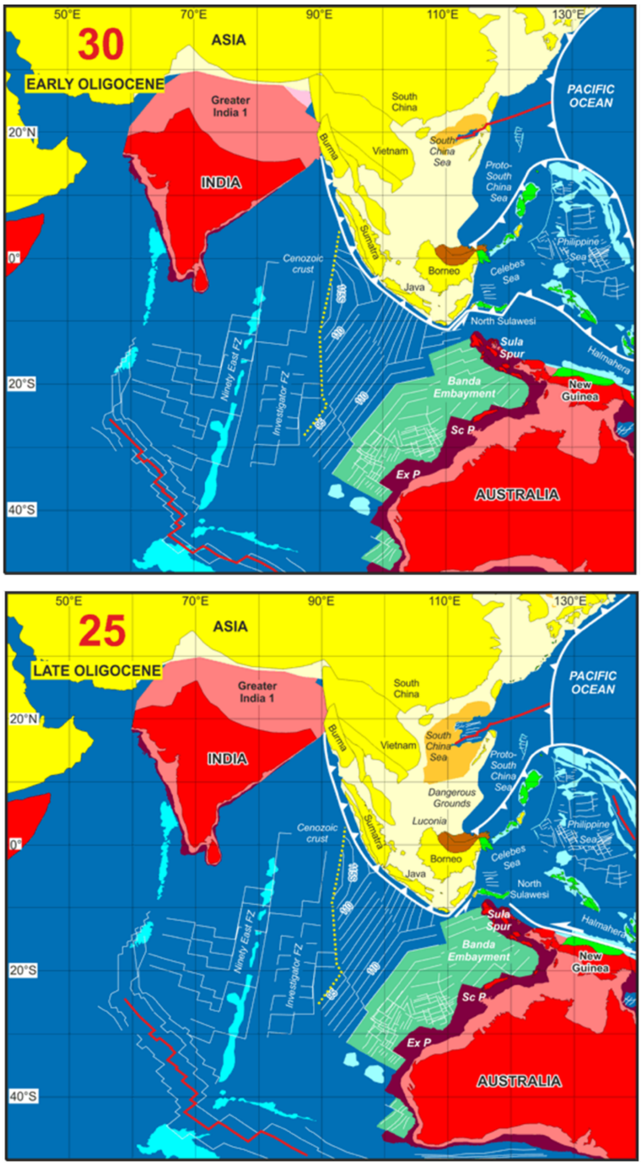

Figure 4.6: The continuing movement of the Indian plate into the Eurasian plate during the Oligocene (Hall, 2012).

The Oligocene brought the end of the Paleogene epoch, giving way to the Neogene. At this time Greater India had crossed into the temperate belt while peninsular India remained in the tropical belt (Figure 4.6). By the end of the Paleogene the Indian subcontinent had been subjected to several climatic changes (Kooyman et al., 2019; Morley, 2018). Fossil evidence has been found for the angiosperm families *Annonaceae*, *Ebenaceae*, *Lauraceae*, and *Sapotaceae* (amongst others) from between the Paleocene and the Oligocene in India (Bhatia et al., 2021). Unlike the Eocene, temperatures in the Oligocene dropped as the world witnessed a period of cooling, which in the tropical belt translates to aridification (Dupont-Nivet et al., 2007), however temperatures remained stable and viable enough for the growth of angiosperms in the tropical belt (Burnham and Morley, 2000; Li et al., 2018). The increased aridity within the subcontinent (Gorin et al., 2020) was not so widespread that wet forests through the subcontinent were completely lost, as evidenced by the results of this study showing immigration of wet forest taxa in this epoch.

Seven clades were found arriving to the Ghats in the Oligocene. The clades belonged to the families – *Dipterocarpaceae*, *Ebenaceae*, and *Sapotaceae*. Dispersal events were scattered throughout the Oligocene. Three clades of *Dipterocarpaceae* (IX, IV, and VII) arrived to the Ghats c.32, 30, and 26 mya respectively. The three clades arrived from Continental Asia and the Sunda Shelf, where *Dipterocarpaceae* had become dominant after their dispersal from the Indian subcontinent (Sanil et al., 2022). Three clades of *Diospyros*, *Ebenaceae* (III, V, and VII) arrived to the Ghats from Continental Asia and Sunda, approximately 29, 28, and 25 mya respectively. A single clade of the animal dispersed tree family *Sapotaceae* (III) arrived to the Western Ghats in the Late Oligocene approximately 26 mya.

Prior to its collision with Tibet, the subcontinent boasted a per humid climate, the perfect haven for the expansion of angiosperms (Morley, 2018; Sen et al., 2019). The collision and subsequent uplift of the Himalayas along with its partial position in the temperate zone saw the per humid climate become a more seasonal one (Gorin et al., 2020). The arrival of these seven clades to the Ghats throughout the Oligocene from the ancestral areas of Continental Asia and the Sunda Shelf is evidence of a constant exchange occurring between the Indian subcontinent and the rest of Asia. In the Oligocene the predominant method of clade dispersal was likely migration via a land bridge/corridor, or short distance dispersal. From the end of the Oligocene through the Miocene to the Pliocene, the Western Ghats saw the arrival of the bulk of angiosperm clades as evidenced by this study.

Miocene (23.03 – 5.33 million years ago)

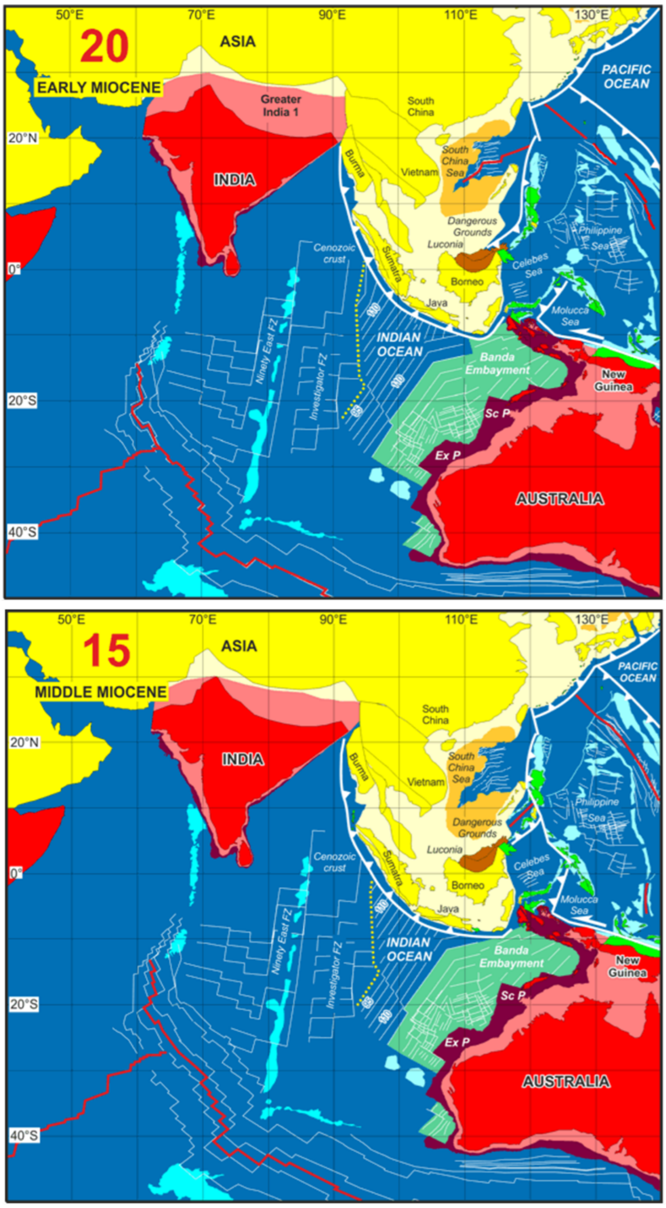

Figure 4.7: The final suturing of the Indian plate with the Eurasian plate in the Miocene (Hall, 2012).

Global temperatures rose during the Miocene driving the world into a thermal maximum (Morley, 2018). India's position in both the temperate and tropical belt, indicate that parts of the subcontinent (Figure 4.7) had a seasonal climate while other parts had a wet per humid climate (Burnham and Morley, 2000), further cause for the Western Ghats having become a refugia for the remaining wet forests of the subcontinent (Johnson et al., 2022; Prasad et al., 2009). The continued rise of the Himalayas in the Miocene also resulted in formation of the South Asian monsoon, a climatic factor responsible for the retention of these per humid temperatures in specific niches (Ashton, 2017; Bhatia et al., 2021; Morley, 2003).

This geological epoch saw the highest number of arrivals into the Ghats. Predominantly from the regions of Continental Asia and the Sunda Shelf. Out of the 49 clades that arrived, only a few had the ancestral ranges of Africa, Sri Lanka, Sahul, and Australia. Dispersal events occurred into the Ghats for all fifteen families addressed in this study. From the Northeast and the East, 16 clades arrived from Continental Asia, 13 from the Sunda Shelf, two from the Sahul Shelf, two from China, and one from the Himalayas. From the West and Southwest of the Ghats, four clades arrived from Africa and one from Madagascar. Finally, from the South, three clades arrived from Sri Lanka. The ancestral area reconstructions found six clades arriving from more than one area. A single clade of *Lauraceae* (I) arrived from the regions of America, China, and Continental Asia. Single clades of *Rubiaceae*, *Piperaceae*, and *Celastraceae* arrived from the regions of Continental Asia, and the Sunda and Sahul Shelves. A single clade of bird dispersed *Loranthaceae* arrived from Australia and the Sunda Shelf. The arrival of angiosperms to the Ghats in the Miocene was evenly distributed throughout the epoch.

The arrival of extant angiosperms in the Ghats predominantly in the Miocene may be attributed to the following occurrences during the epoch – (i) The Indian subcontinent was witnessing the spread of an arid climate – this was largely due to the formation and continued uplift of the Himalayas, (ii) the Northern half of India sat in the seasonal latitudes, (iii) the formation of the South Asian monsoon in the late Oligocene-Miocene, (iv) the Miocene thrust global temperatures into that of a thermal maximum, (v) the Western Ghats behaving as a barrier preventing precipitation over central India. These are all factors leading to a retention wet forest taxa in the last remaining wet forests on the subcontinent (the Ghats) aside from the Himalayas and the Eastern Ghats. So, while the Eocene-Oligocene may have been the period for mass dispersal events into India from the rest of Asia, the Miocene marked the dispersal into and turnover of the flora of the Western Ghats. Similar patterns of Miocene arrival were found in studies that focused on the families *Piperaceae* and *Myrtaceae* in the region (Rajasri et al., 2020; Sen et al., 2019).

The only other remaining wet forests on the Indian subcontinent are in the Himalayas and partly the Eastern Ghats. However, the Himalayas unlike the Western Ghats are a much younger range, that have a functionally and floristically different flora and do not appear to share forest composition or diversity (Chitale et al., 2014). From the point of uplift to the end of the Pleistocene, only two clades in this study were seen arriving to the Ghats from the Himalayas. This low signal from the Himalayas is intriguing, as their relative nearness in comparison to that of the Sunda Shelf or Continental Asia would suggest the Ghats see more arrivals of Himalayan taxa, yet there is evidence of only two clades, both herbs. This floristic difference between the Himalayas and the Western Ghats may be attributed to two things – (i) the aridity of central India – effectively becoming an impossible dispersal barrier to cross and (ii) climatic variability – the Himalayas lie in the temperate zone with more pronounced seasonal changes – implying that the flora of the range is not well adapted to the wet tropical climate which predominates in the Ghats. Hence, we see more arrivals from the climatically similar Continental Asia and Sunda Shelf. There however is evidence of disjunct populations of *Rhododendron arboreum* in both the Western Ghats and the Himalayas; this is a higher montane genus and may be in a niche space which is more similar between the two ranges (Kuttapetty et al., 2014). A similar occurrence is seen for the clade *Begoniaceae* II. The clade consisted of four taxa – *Begonia trichocarpa*, *Begonia phrixophylla*, *Begonia concanensis,* and *Begonia picta*. *Begonia concanensis and Begonia phrixophylla* are Western Ghats endemics, *Begonia trichocarpa* is native to both the Ghats and the Himalayas, and *Begonia picta* is endemic to the Himalayas. The clade shows recent dispersal into the Ghats in the Late Miocene, with a signal from the Himalayas.

Connections between the Western Ghats and the Eastern Ghats are something to be explored as well. Unlike the Himalayas and the Western Ghats, the Western Ghats and the Eastern Ghats are connected by land bridges of sorts, commonly referred to as elephant corridors, in the Nilgiri Biosphere Reserve (Daniels, 1996). These land bridges provide excellent connections for migration or short distance dispersal. There is evidence of shared taxa of *Annonaceae, Acanthaceae,* and *Rubiaceae* between the Western and Eastern Ghats (Davidar, 2009). There is also evidence of dispersal events of the centipede genus *Ethmostigmus* occurring into and out of the Western Ghats to the Eastern Ghats (Joshi and Edgecombe, 2019).

Pliocene (5.33 – 2.58 million years ago)

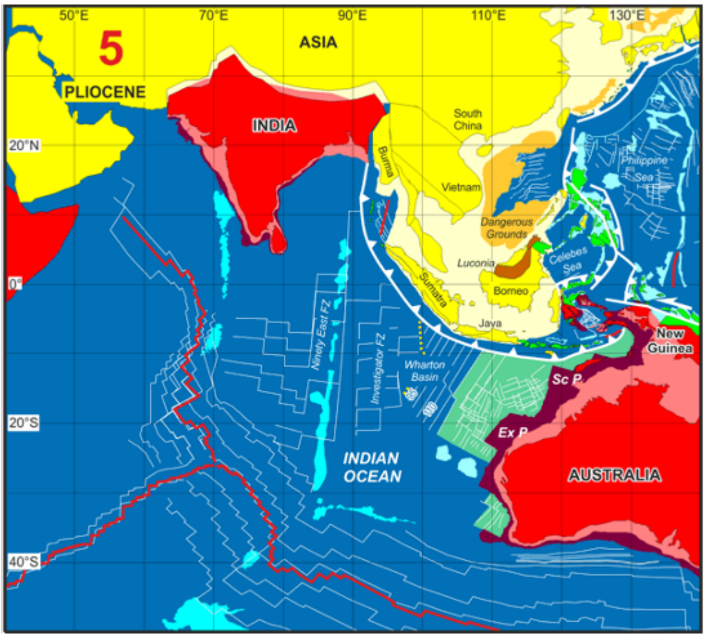

Figure 4.8: The formation of the Himalayas and India’s continued collision with Eurasia in the Pliocene (Hall, 2012).

The Miocene-Pliocene boundary was once again a time of global cooling, in the tropics this translated as increased arid and seasonal climate (Dupont-Nivet et al., 2007). India occupied the same space in the Pliocene as it does today (Figure 4.8). Unlike the Oligocene, the Pliocene saw the subcontinent becoming effectively dry with wet forests more or less disappearing from the centre (Burnham and Morley, 2000). The retention of megathermal angiosperm clades in surviving per humid niches of the Indian subcontinent (Morley, 2003), effectively increased the biodiversity quotient of the Western Ghats in comparison to the rest of the subcontinent.

The Pliocene saw the arrival of 14 clades to the Ghats, nine belong the rhizomatous herb family *Zingiberaceae*. Clades of the ginger family arrived from Continental Asia, China, Sri Lanka, and the Sunda Shelf. The increased arrival of *Zingiberaceae* in the Pliocene when compared to the Miocene was also found in a recent study of the family (Zhao et al., 2022). Three clades of *Annonaceae* arrived from Continental Asia and the Sunda Shelf, and one clade of *Begoniaceae* arrived from the Sunda Shelf. One clade of *Orchidaceae* arrived to the Ghats from several ranges in Asia – the Himalayas, China, Continental Asia, and the Sunda Shelf. Dispersal once again being the favoured method of range expansion for the flora in this geological age. A study on *Rhododendron arboreum* found evidence of within-species disjunction between the Himalayas and the Southern Western Ghats, potentially indicating that the subcontinent had more wet forest expanses and corridors connecting them to each other during climatic cycles (Kuttapetty et al., 2014). This is known as the Satpura Hypothesis, which suggests that the Satpura range in central India behaved as a perhumid corridor between the Himalayas and the Western Ghats during the Pleistocene glaciation period (Hora, 1953).

Pleistocene (2.58 – 0.017 million years ago)

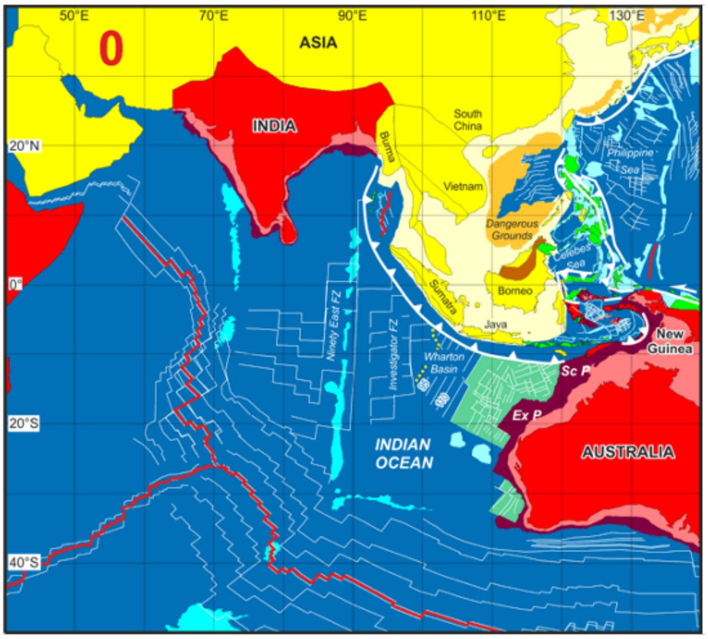

Figure 4.9: The subcontinent of India, Continental Asia, and Southeast Asia as we know them today (Hall, 2012).

The Pleistocene was the start of the Quaternary and a period of extreme climates (Burnham and Morley, 2000). It has been suggested that the multiple glacial and interglacial periods of this epoch were responsible for the loss of the subcontinent's tropical diversity (Prasad et al., 2009) (Figure 4.9). The glacial and interglacial periods would have induced several range expansions and contractions and subsequently the loss of flora (Connor, 1986). Global cooling would have been seen as aridity in the tropics, implying that the number of opportunities for dispersal of wet forest flora would be much fewer (Burnham and Morley, 2000). Only two clades of the 75 arrived into the Ghats during this epoch. Both clades belonged to the monocot family *Zingiberaceae.*

One clade arrived from Continental Asia, while the second arrived from Sri Lanka. The island of Sri Lanka and the Western Ghats together combine to form one of the world's biodiversity hotspots (Gunawardene *et al.*, 2007). Dispersals from Sri Lanka are likely to have occurred via the Palk Strait, a land bridge that became subaerial in the Pleistocene (Bossuyt, 2004). Considering its latitudinal position this land bridge would have been dominated by savannahs or scrub forests (Burnham and Morley, 2000) similar to those of today (Meegaskumbura et al., 2019). However, while there exists a connection between the Ghats and Sri Lanka, there is abundant evidence indicating that they have noticeably different floras (Bossuyt, 2004; Gunawardene et al., 2007; Van Bocxlaer et al., 2012). In addition to which of the 75 clades that arrived to the Western Ghats only 6 showed a signal of origin from Sri Lanka.

The Western Ghats Today

Diversity in the Ghats is relatively young and appears to have arrived via geologically recent immigration, with floristic links to Continental and Southeast Asia rather than the rest of the Indian subcontinent or the Himalayas. Based on contemporary temperature seasonality and annual precipitation levels, we see similar climate niches in the Western Ghats, Continental Asia, and the Sunda Shelf (Figures 4.10 & 4.11). This is congruent with a hypothesis of climatic similarity driving the observed floristic similarity, and dispersal being the main influence for the composition of the flora. The Ghats are the first hurdle encountered by the South Asian monsoon (Gunnell, 1997), a system that supports the retention of their pre-collision per humid forests, providing a climatic analogue to areas with evergreen wet tropical forests in other parts of Asia. When the Indian plate collided with the Tibet, it created an arid zone through the centre of the subcontinent, now referred to as the Deccan plateau. Leaving the Western Ghats, the Himalayas and parts of the Eastern Ghats as the last harbourers of pre-collision wet forests (Morley, 2003).

While the Western Ghats are a part of the Indian peninsula, their latitudinal position and encounters with the South Asian monsoons result in an entirely unique climatic environment found no-where else on the subcontinent (Prasad et al., 2009). This comparatively small climatic niche is home to a vast range of flora, much of which is entirely unique to the range and contains signals from ca. 50 My of floristic exchange. The size of the Ghats and the effect of climate change on this range will have damaging consequences to the biodiversity of the Indian subcontinent – losing both new and potentially old flora.

The results of this study have added to the current understanding of floristic Phylogenetic Diversity (PD) in the Western Ghats. Further study of the phylogenetic diversity of the range will aid in the identification of areas of high lineage diversity as well as regions of stable climate optimum for floristic refugia. By analysing PD in terms of the Ghats' unique climate it is possible to protect regions of the range with high diversity that require conservation, as indicated in a recent study conducted in the Ghats (Gopal et al., 2023).

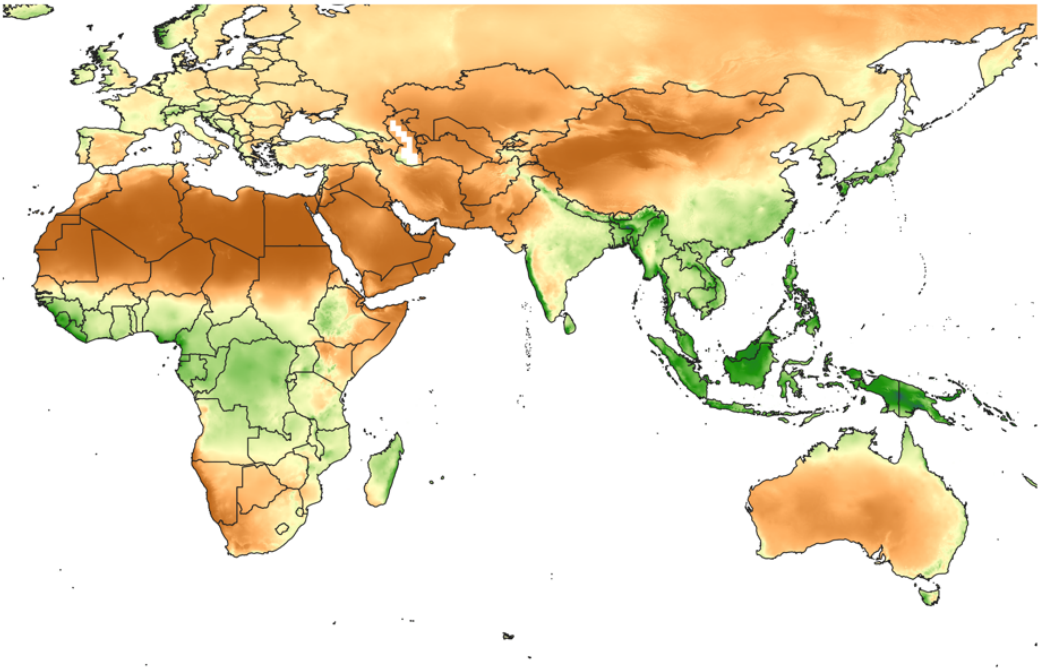

Figure 4.10: Annual precipitation in the world. Shades of green depicting areas with higher rates of precipitation than those in brown.

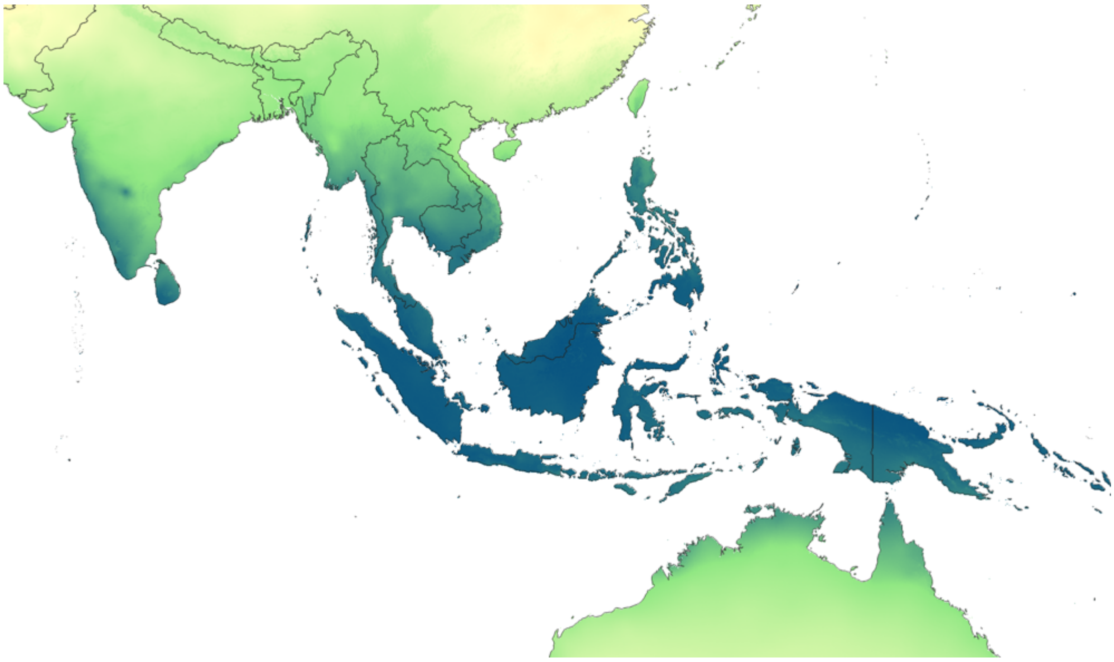

Figure 4.11: Temperature seasonality over Asia. Blue shades depict decreasing temperature seasonality.

4.3 Conclusions

The Western Ghats, also known as the Sahyadri mountain range or the Great Escarpment of India, are an ancient and discontinuous mountain range. All these names aside they stand to be one of the most distinct mountain ranges in the world, and they come with an exceptionally fascinating bio(geo)graphy.

The extant angiosperm flora of the Ghats arrived predominantly during the Miocene with mostly Continental Asian and Sunda Shelf origins, and indicates that our data fits the hypothesis of dispersal into of India, post collision of the subcontinent with Asia. The tumultuous nature of India's journey through the latitudes, its encounters with climate change, severe volcanism, meteor collisions, and its ultimate collision with the rich flora on the Eurasian plate mean vicariant floristic remnants are not detectable in the Western Ghats extant flora.

This study found no dispersal events into the Western Ghats from the Early Cretaceous to the Late Paleocene. India's movement through the latitudes into the Northern Hemisphere indicates that at some point in the Cretaceous it was in the Mediterranean belt (Chatterjee et al., 2013), implying it was witness to aridification which would not suit a wet megathermal flora on the subcontinent. It is likely that due to its turbulent geological history, global climatic changes and its movement through the latitudes, the Western Ghats witnessed widespread species composition turnover over the span of 100 million years, starting with a Gondwanan flora, witnessing mass extinctions and then immigration and colonisation by a younger more resilient flora. This is supported by a recent study comparing the phylogenetic diversity of Indian and Malagasy rainforest floras, showing the proportion of shared lineages decreased through geological time after the rifting of India (Barthelemy et al., 2022).

Although the results of this study largely favour the arrival of angiosperms in the Miocene from Asia, there is some evidence for taxa having rafted on the Indian subcontinent, such as for *Dipterocarpaceae* and *Zingiberaceae*. Although not replicated here, Sanil et al. (2022) found a likely Gondwanan vicariant origin for Dipterocarpaceae, which is also represented by a fossil dating to c.52 mya on the subcontinent. Rafting post-split of Gondwana has been postulated for having a role in the colonisation of Asia by *Zingiberaceae* due to fossils present in the Deccan traps, however this is not backed up by molecular phylogenies of extant taxa in this or other studies (Zhao et al., 2022). The presence of *Crypteroniaceae* in Southeast Asia and Sri Lanka (but not on the Indian subcontinent) has also been cited as evidence of Gondwanan vicariance (Conti et al., 2002; Karanth, 2006), but further work is needed on the molecular dating of this. The fossil evidence shows that although the flora of India would have been transformed and traumatised during the subcontinents journey, it would never have been entirely extirpated. The lack of phylogenetic signal of this in the extant flora is likely due to extinction and over-writing of past vicariance through mass floristic exchange with climatically similar areas in Asia. However, there is a clearer evidence of faunal relics still existing today, supported by phylogenetic data (Dutta et al., 2004; Johnson et al., 2022; Joshi and Edgecombe, 2019; Van Bocxlaer et al., 2012). That animal clades have retained some older and demonstrably vicariant lineages whilst plants have not is best explained by the dispersal abilities of angiosperms leading to a blurring of past distributions.

The cradle versus museum hypothesis of tropical diversity has been the source of much debate, it is a dichotomy. The concept of cradle vs museum does not examine the deep evolutionary processes involved in the arrival or extinction of species in tropical rainforests (Vasconcelos et al., 2022). As evidenced by this study, the geological and climatic histories of ranges are vital to the understanding of their respective bio-diversities, it is not simply enough to classify a rainforest as museum or cradle based on the age of their species compositions alone. Similar studies tracing the arrival of angiosperm lineages through time and space have been conducted in the regions of Sri Lanka, the Sunda and Sahul shelves, and the Neotropics (Crayn et al., 2015; unpublished, Kumarage, 2016; Vasconcelos et al., 2020). A study conducted in a similarly ancient range, the Campos rupestres, in Brazil found that despite the geological age of the ridge, the flora of the region was quite young (Vasconcelos et al., 2020).

Despite the vastly different age and tumultuous history of the Ghats, it seems in many ways they have a flora not so dissimilar from other tropical montane floras, consisting of geologically youthful lineages, and driven by dispersal and high species turnover.

4.4 Further Research

The flora of the Western Ghats is vast, and this study only manages to address a percentage of its extensive biogeographic history. Further sampling would help establish the concept of a relatively young flora. The addition of other angiosperm families would improve our understanding of whether the flora of the Ghats is truly young or if some Gondwanan relics remain as seen in the fauna of the region. This study has some data for the family *Gesneriaceae* which needs further analysis. Other families to choose from would be those for which fossil evidence has previously been found on the Indian subcontinent, as well as those families that rose to dominance in the forests of Continental and Southeast Asia.

The data generated for *Begonia* in this study consisted of multiple samples of each species and phylogenies from all three genome compartments. The taxonomic clarification of names in the nomenclaturally complex cane *Begonia*s of the Western Ghats is currently a work in progress, as is understanding the phylogenetic incongruence of taxa seen amongst chloroplast, nuclear, mitochondrial trees.

Further work is also needed on the Bioinformatics problem that is soft clipping. This study observed the removal of good and useful reads from shallow whole genome skims during inspection of individual BAM files, and would be useful to understand whether similar issues arise when these mapping packages are employed for bait capture data, and whether there is a noticeable difference in the subsequent consensus' that are called.

In terms of biogeography, investigating the dispersal syndromes and niche envelopes of the species in the families studied here would give greater understanding of differences in the number of dispersal events and the area of origin between families. The Ghats are not homogenous, and looking at niche evolution in the families which represent different functional types and are present in different altitudinal ranges may help to better explain the build up of the flora. An empirical analysis of climatic similarity of the Ghats and surrounding areas of origin would also be beneficial. This study comprehensively looked at clades and species arriving into the Ghats. This could be extended into a study looking at floristic exchange between all regions in the project, especially regarding exchange involving out-of-India dispersal. This could be done using stochastic mapping as implemented in BioGeoBEARS (Matzke, 2018). Finally, the biogeographic analyses could be further exptended using a statified analysis which includes information on past area configuration and connection (e.g., (Baker et al., 2020)) which may help highlight any signal of vicariant events.

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Appendix

A.1 Sample set

Taxon Name	**Collector Name(s)**	**Collecto Number**	**Country**	**Material Type**	**Herbarium**	**User DNA ID**	**Herbarium Barcode**	**Location**	**Collection Date**	**Sample name in phylogeny**	**Lab Protocol**	**Qubit ng/µL**	**Nano Drop ng/µL**		**Notes**
									Annonaceae						
Annona reticulata	Robert Wight	23 or 26	IN	H	E	MAno05	E00850284	Courtallam	July 1835	MAno05	WGS	1.82	1.2	MAno05	
Polyalthia cerasoides	Robert Wight		IN	H	E	MAno06	E00850279	Courtallam	July 1835	MAno06	WGS	8.775	2.1	MAno06	
Uvaria narum	Robert Wight		IN	H	E	MAno08	E00850277	Quilon (Kollam)	June 1836	MAno08	WGS	3.96	2.08	MAno08	
Desmos lawii	Robert Wight		IN	H	E	MAno12	E00850278	Quilon (Kollam)	June 1836	MAno12	WGS	0.026	2.02	MAno12	
Annona reticulata	Madhavi Sreenath	MASR038	IN	SD		MSF16		Mukkali, Bhavani Range Gate, Silent Valley National Park	22-Aug-22	MSF16	WGS	1.37	2.01	MSF16	
Miliusa tomentosa	C J Saldanha	14112	IN	H	E	MAno10	E00092513		July 16 1969	MAno10	WGS	0.951	1.74	MAno10	
Goniothalamus rhynchantherus	Robert Wight	12	IN	H	E	MAno01	E00850281		September 1835	*Goniothalamus_rhynchantherus_MAno01*	WGS	0.88	3.8	MAno01	
Goniothalamus cardiopetalus	A S Rao	85594	IN	H	E	MAno02	E00850282	Abbi Falls stream, Coorg District		*Goniothalamus_cardiopetalus_MAno02*	WGS	2.525	2.45	MAno02	
Goniothalamus wightii	Robert Wight		IN	H	E	MAno03	E00179455	Courtallam	February 1836	*Goniothalamus_wightii_MAno03*	WGS	0.022	1.66	MAno03	
Orophea uniflora	Robert Wight	7	IN	H	E	MAno04	E00393099	Courtallam	July 1835	*Orophea_uniflora_MAno04*	WGS	0.759	57.41	MAno04	
Polyalthia suberosa	Robert Wight	19	IN	H	E	MAno07	E00850280	Courtallam	March 1835	*Polyalthia_suberosa_MAno07*	WGS	5.745	2.04	MAno07	
Miliusa wightiana	Robert Wight	17	IN	H	E	MAno09	E00092507	Peninsular India Orientalis		*Miliusa_wightiana_MAno09*	WGS	3.885	2.18	MAno09	
Miliusa indica	Robert Wight	13	IN	H	E	MAno11	E00206708		September 1835	*Miliusa_indica_MAno11*	WGS	5.245	2.08	MAno11	
Mitrephora heyneana	Commander J Campbell		IN	H	E	MAno13	E00850283	Pulney Mountains	September 1836	*Mitrephora_heyneana_MAno13*	WGS	3.47	2.24	MAno13	
Polyalthia longifolia	Madhavi Sreenath	MASR021	IN	SD		MSF12		Range Forest Office, Somwarpet		*Polyalthia_longifolia_MSF12*	WGS	9.46	2.15	MSF12	
Artabotrys zeylanica	Madhavi Sreenath	MASR023	IN	SD		MSF27		Devarkadu, Shantahalli, Somwarpet Range	18-Aug-22	*Artabotrys_zeylanica_MSF27*	WGS	1.38	2.19	MSF27	

Taxon Name	Collector Name(s)	Collecto Number	Country	Material Type	Herbarium	User DNA ID	Herbarium Barcode	Location	Collection Date	Sample name in phylogeny	Lab Protocol	Qubit ng/µL	Nano Drop ng/µL		Notes
							Begoniaceae								
Begonia dipetala	Robert Wight		IN	H	E	BDi02	E00300339	Courtallam		BDi02	WGS	1.675	1.94	BDi02	
Begonia dipetala	H F Cleghorn and sq M D		IN	H	E	BDi04	E00300512	Anamallay (Anamalai)	1859	BDi04	WGS	0.271	1.77	BDi04	
Begonia dipetala	Robert Wight	839	IN	H	E	BDi05	E00300338	Courtallam		BDi05	WGS	0.149	0.97	BDi05	
Begonia dipetala	Nathaniel Wallich	3675 D	IN	H	E	BDi06	E00300347	Nilgherry (Nilgiri Hills)		BDi06	WGS	0.134	1.46	BDi06	
Begonia dipetala		794	IN	H	E	BDi09	E00300345	Pykara Falls	December 23 1986	BDi09	WGS	0.883	1.55	BDi09	
Begonia dipetala			IN	H	E	BDi12	E00300340	Conoor, Nilgiri Hills		BDi12	WGS	0.118	1.6	BDi12	
Begonia dipetala	Robert Wight		IN	H	E	BDi15	E00300343	Courtallam	July 1835	BDi15	WGS	1.87	1.11	BDi15	
Begonia dipetala		1795/1792	IN	H	E	BDi16	E00300334	Peninsular India Orientalis		BDi16	WGS	0.327	1.02	BDi16	
Begonia dipetala	H F Cleghorn and sq M D		IN	H	E	BDi18	E00300331	Neilgherry Hills	1855	BDi18	WGS	1.82	1.88	BDi18	
Begonia dipetala	Robert Wight	1795	IN	H	E	BDi19	E00300335	Peninsular India Orientalis		BDi19	WGS	2.02	1.31	BDi19	
Begonia dipetala	Robert Wight	1794	IN	H	E	BDi20	E00300413	Peninsular India Orientalis		BDi20	WGS	0.313	1.82	BDi20	
Begonia dipetala (Begonia hydrophila)			IN	H	E	BDi21	E00300333	Nilgiri Mountains		BDi21	WGS	6.655	1.96	BDi21	
Begonia dipetala	George Watt		IN	H	E	BDi22	E00300346	Nilghiri Hills		BDi22	WGS	0.912	1.93	BDi22	
Begonia dipetala	Edward Barnes	199	IN	H	K	BDi23		Nilgiris	01/06/1933-June 1933	BDi23	WGS	3.536	1.76	BDi23	
Begonia dipetala	C E Ridsdale	682	IN	H	K	BDi24		Devicolam - Periyar Road	24/03/1980	BDi24	WGS	3.105	1.7	BDi24	
Begonia dipetala	L Anglade	10659	IN	H	K	BDi26		Pulney Hills	Jul-26	BDi26	WGS	5.155	1.86	BDi26	
Begonia dipetala	Ridsdale	717700486	IN	H	K	BDi27	K717700486	Above Courtallum, 800m	16/01/1979	BDi27	WGS	9.36	1.89	BDi27	
Begonia malabarica	Robert Wight		IN	H	E	BMa1	E00179313	Courtallam	September 1835	BMa1	WGS	0.099	0.82	BMa1	
Begonia malabarica	Robert Wight	838	IN	H	E	BMa10	E00179307	Courtallam	February 1836	BMa10	WGS	1.975	2	BMa10	
Begonia malabarica	Robert Wight		IN	H	E	BMa11	E00179306	Courtallam	July 1835	BMa11	WGS	6.55	1.94	BMa11	

Taxon Name	Collector Name(s)	Collecto Number	Country	Material Type	Herbarium	User DNA ID	Herbarium Barcode	Location	Collection Date	Sample name in phylogeny	Lab Protocol	Qubit ng/µL	Nano Drop ng/µL		Notes
Begonia malabarica	Robert Wight	836	IN	H	E	BMa15	E00179316	Malabar		BMa15	WGS	1.37	1.95	BMa15	
Begonia malabarica	Robert Wight		IN	H	E	BMa16	E00179308	Courtallam	August 1835	BMa16	WGS	0.248	1.03	BMa16	
Begonia brevicaulis	G H Cave		IN	H	E	MBeg02	E00157125	Tista	01-Aug-17	MBeg02	WGS	1.175	1.88	MBeg02	Extracted twice
Begonia concanensis		51 or 57	IN	H	E	MBeg10	E00022097	Lonavala (Lanowlee)	August	MBeg10	WGS	1.395	1.54	MBeg10	Extracted twice
Begonia sp	G Watt	10237	IN	H	E	MBeg11	E00300511	Poona Ghat	August 16 1891	MBeg11	WGS	0.307	1.47	MBeg11	
Begonia trichocarpa	Mr. Law		IN	H	K	MBeg14		Bababudan Hills, Malabar	1872	MBeg14	WGS	1.405	1.07	MBeg14	
Begonia thwaitesii	Philcox and Weerasooriya	10748	IN	H	K	MBeg15		Matale District, Rattota to Illukkumbura road	11/02/1996	MBeg15	WGS	0.357	1.31	MBeg15	
Begonia fallax	Col. Beddome		IN	H	K	MBeg17		South Canara to Ceylon	December 1880	MBeg17	WGS	2.225	1.68	MBeg17	
Begonia trichocarpa	Nikhil Krishna and Pradip VD	148480	IN	SD	C	CUBG12		Morjai Plateau		CUBG12	WGS	1.885	1.87	CUBG12	Extracted twice
Begonia concanensis	W A Talbot	783	IN	H	E	MBeg03	E00022098	Some area in North Kanara	December 4 1883	MBeg03	WGS	0.775	1.53	MBeg03	Extracted twice
Begonia brevicaulis	G H Cave		IN	H	E	MBeg08	E00300429	Tista	21-Jul-15	MBeg08	WGS	0.437	1.4	MBeg08	Extracted twice
Begonia floccifera	Anonymous	10842	IN	H	K	MBeg13		Sengalteri, Tinnevely	Oct-19	MBeg13	WGS	0.662	1.7	MBeg13	Extracted twice
Begonia dipetala	Robert Wight	695	IN	H	E	BDi01	E00300342	Courtallam	March 1835	BDi01	WGS	0.063	0.98	BDi01	
Begonia dipetala	Robert Wight	2793	IN	H	E	BDi07	E00300341	Peninsular India Orientalis		BDi07	WGS	0.06	2.92	BDi07	
Begonia dipetala	Robert Wight	1795	IN	H	E	BDi10	E00300417	Peninsular India Orientalis		BDi10	WGS	0.026	1.11	BDi10	
Begonia dipetala		795	IN	H	E	BDi11	E00300349	Kartairy	14 May 1889	BDi11	WGS	0.086	1.07	BDi11	
Begonia dipetala	Robert Wight	1796	IN	H	E	BDi13	E00300332			BDi13	WGS	0.006	-3.38	BDi13	
Begonia dipetala	Robert Wight		IN	H	E	BDi14	E00300350	Peninsular India Orientalis		BDi14	WGS	0.018	1.89	BDi14	
Begonia dipetala	Robert Wight	1799	IN	H	E	BDi17	E00300418	High Hills		BDi17	WGS	0.14	1.83	BDi17	
Begonia malabarica	Robert Wight	698	IN	H	E	BMa2	E00179314	Courtallam	September 1835	BMa2	WGS	0.208	2.47	BMa2	
Begonia malabarica	Robert Wight		IN	H	E	BMa3	E00179315	Courtallam	September 1835	BMa3	WGS	0.231	1.9	BMa3	

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Begonia malabarica	Robert Wight		IN	H	E	BMa4	E00179312	Courtallam	September 1835	BMa4	WGS	0.398	1.61	BMa4	
Begonia malabarica	Robert Wight	696	IN	H	E	BMa5	E00179309	Courtallam	August 1835	BMa5	WGS	0.086	0.82	BMa5	
Begonia malabarica	Robert Wight		IN	H	E	BMa6	E00179311	Courtallam	August/September 1835	BMa6	WGS	0.32	1.49	BMa6	
Begonia malabarica	Robert Wight		IN	H	E	BMa7	E00179310	Courtallam	August 1835	BMa7	WGS	0.004	-4.38	BMa7	
Begonia malabarica	Colin Ernest Ridsdale	399	IN	H	E	BMa8	E00649103	Walaiyar Estate, Papanasam, Tamil Nadu	July 13 1976	BMa8	WGS	0.032	1.13	BMa8	
Begonia malabarica	Robert Wight		IN	H	E	BMa12	E00179304	Courtallam		BMa12	WGS	0.109	1.01	BMa12	
Begonia malabarica	Robert Wight	837	IN	H	E	BMa14	E00179317	Malabar	June 1836	BMa14	WGS	0.227	0.99	BMa14	
Begonia malabarica	Ridsdale	399	IN	H	K	BMa17		Waliyar Estate, Papanasam	13/07/1976	BMa17	WGS	0.062	1.12	BMa17	
Begonia malabarica	Colin Ernest Ridsdale	144	IN	H	E	BMa19	E00649089	Ponmudi Tea Plantation, Kerala	June 11 1976	BMa19	WGS	0.034	-2.52	BMa19	
Begonia malabarica	Robert Wight		IN	H	E	BMa21	E00300407	Peninsular India Orientalis		BMa21	WGS	0.04	0.41	BMa21	
Begonia malabarica	Robert Wight		IN	H	E	BMa22	E00300414	Peninsular India Orientalis		BMa22	WGS	0.093	0.12	BMa22	
Begonia sp		10237	IN	H	E	MBeg18	E00300509	Kali Caves, Poona (Pune)	August 1891	MBeg18	WGS	0.55	1.84	MBeg18	
Begonia hydrophilla	LJ Sedgwick	7061	IN	H	K	MBeg19		Evergreen near Jog	Oct-19	MBeg19	WGS	0.184	1.26	MBeg19	
Begonia hydrophilla	Ridsdale	283	IN	H	K	MBeg20		Silent Valley, Pulney Hills	25/06/1976	MBeg20	WGS	0.058	1.07	MBeg20	
Begonia dipetala			IN	H	E	BDi08	E00300344			BDi08	WGS	0.227	3.51	BDi08	
Begonia crenata	Stocks, Law		IN	H	E	MBeg04	E00300307	Propé Malabar, Concan		MBeg04	WGS	0.057	1.05	MBeg04	
Begonia sp	Robert Wight	1214	IN	H	E	MBeg09	E00300513	Peninsular India Orientalis		MBeg09	WGS	0.122	-0.89	MBeg09	Extracted twice
Begonia fallax	Ridsdale	68	IN	H	K	MBeg16		Ponmudi Kerala	08/06/1976	MBeg16	WGS	0.03	2.1	MBeg16	
Begonia malabarica	Madhavi Sreenath	MASR001	IN	SD		MSF1		Office of the Deputy Wildlife Warden Madikeri Division	15/08/2022	MSF1	WGS	0.472	2.2	MSF1	
Begonia malabarica	Madhavi Sreenath	MASR010	IN	SD		MSF3		Office of the Deputy Wildlife Warden Madikeri Division	16/08/2022	MSF3	WGS	0.404	1.76	MSF3	

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Begonia malabarica	Madhavi Sreenath	MASR027A	IN	SD		MSF8		Office of the Assistant Wildlife Warden Tholpetty Range, Begur, Wayanad	19/08/2022	MSF8	WGS	2.4	2.14	MSF8	
Begonia malabarica	Madhavi Sreenath	MASR027B	IN	SD		MSF9		Office of the Assistant Wildlife Warden Tholpetty Range, Begur, Wayanad	19/08/2022	MSF9	WGS	0.468	2.06	MSF9	
Begonia malabarica	Madhavi Sreenath	MASR027C	IN	SD		MSF10		Office of the Assistant Wildlife Warden Tholpetty Range, Begur, Wayanad	19/08/2022	MSF10	WGS	1.93	2.19	MSF10	
Begonia cordifolia	Robert Wight	835	IN	H	E	MBeg05	E00013887	Malabar	June 1835	MBeg05	WGS	0.094	4.16	MBeg05	
Begonia arnottiana	Robert Wight	693	IN	H	E	MBeg01	E00179303	Courtallam	September 1835	MBeg01	WGS	0.347	1.92	MBeg01	Extracted twice
Begonia subpeltata	Robert Wight	841	IN	H	E	MBeg06	E00022038	Pavanasam (Papanasam)	January 1836	MBeg06	WGS	0.485	1.58	MBeg06	Extracted twice
Begonia sp	Walker Arnot		IN	H	E	MBeg07	E00300508	Bombay		MBeg07	WGS	0.171	4.25	MBeg07	Extracted twice
Begonia dipetala	Robert Wight		IN	H	E	BDi03	E00300416	Courtallam	July 1835	BDi03	WGS	0.539	2.15	BDi03	
Begonia dipetala	Thwaite	3949	IN	H	K	BDi25				BDi25	WGS	0.277	4.31	BDi25	
Begonia malabarica	Robert Wight		IN	H	E	BMa9	E00300405	Peninsular India Orientalis		BMa9	WGS	4.8	1.88	BMa9	
Begonia malabarica	Mr Woodrow		IN	H	E	BMa20	E00300514	Poona		BMa20	WGS	0.25	3.7	BMa20	
Begonia malabarica	AG Robyns	7181	IN	H	K	BMa23		Hantane, East Slope, Kandy District	15/02/1971	BMa23	WGS	1.545	1.63	BMa23	
Begonia dipetala	Madhavi Sreenath	MASR040B	IN	SD		MSF15		Bhavani Range, Silent Valley National Park, Karuvar	23/08/2022	MSF15	WGS	0.85	2.18	MSF15	
Begonia anaimalaiensis	Madhavi Sreenath	MASR034	IN	SD		MSF17		Mukkali, Bhavani Range, Silent Valley	22/08/2022	MSF17	WGS	2.66	2.11	MSF17	

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Begonia anaimalaiensis	Madhavi Sreenath	MASR036A	IN	SD		MSF19		Mukkali, Bhavani Range, Silent Valley	22/08/2022	MSF19	WGS	2.76	1.96	MSF19	
Begonia anaimalaiensis	Madhavi Sreenath	MASR035	IN	SD		MSF22		Mukkali, Bhavani Range, Silent Valley	22/08/2022	MSF22	WGS	2.7	2.15	MSF22	
Begonia dipetala	Madhavi Sreenath	MASR053	IN	SD		MSF41		Bhavani Range, Silent Valley National Park	23/08/2022	MSF41	WGS	2.34	2.21	MSF41	
Begonia fallax	Nikhil Krishna	168402	IN	SD	C	CUBG1		Agasthyamala		CUBG1	WGS	1.985	2	CUBG1	
Begonia malabarica	Nikhil Krishna	168433	IN	SD	C	CUBG3		Malappuram		CUBG3	WGS	7.525	1.87	CUBG3	
Begonia dipetala	Nikhil Krishna	148492	IN	SD	C	CUBG4		Yercaud		CUBG4	WGS	12.45	2.02	CUBG4	
Begonia hydrophila	Nikhil Krishna	148451	IN	SD	C	CUBG5		Bagamandala		CUBG5	WGS	6.09	2.07	CUBG5	
Begonia hydrophila	Nikhil Krishna	148441	IN	SD	C	CUBG9		Kakkayam		CUBG9	WGS	2.005	1.89	CUBG9	
Begonia fallax	Nikhil Krishna	148471	IN	SD	C	CUBG10		Goodrikal		CUBG10	WGS	1.475	1.86	CUBG10	
Begonia dipetala	Nikhil Krishna	168435	IN	SD	C	CUBG11		Calicut University Botanic Garden		CUBG11	WGS	1.665	1.95	CUBG11	
Begonia malabarica	Nikhil Krishna	148459	IN	SD	C	CUBG13		Pooyamkuty		CUBG13	WGS	4.91	2.04	CUBG13	
Begonia hydrophila	Nikhil Krishna	168434	IN	SD	C	CUBG14		Calicut University Botanic Garden		CUBG14	WGS	4.8	1.96	CUBG14	
Begonia sp	Nikhil Krishna	148442	IN	SD	C	CUBG15		Kakkayam		CUBG15	WGS	66	2.04	CUBG15	
Begonia sp	Nikhil Krishna	168410	IN	SD	C	CUBG16		Thenjhipalam		CUBG16	WGS	8.325	2.01	CUBG16	
Begonia sp	Madhavi Sreenath	MASR032	IN	SD		MSF18		Office of the Assistant Wildlife Warden Tholpetty Range, Begur, Wayanad	19/08/2022	MSF18	WGS	3.34	2.14	MSF18	
Begonia malabarica	Mr Woodrow		IN	H	E	BMa20	E00300514	Poona		BMa20	WGS	0.25	3.7	BMa20	
Begonia concanensis	Drisya	148438	IN	SD	C	CUBG2		Agumbe		*Begonia_concanensis_CUBG2*	WGS	0.17	1.33	CUBG2	
Begonia malabarica	Robert Wight		IN	H	E	BMa18	E00300410	Peninsular India Orientalis		*Begonia_malabarica_BMa18*	WGS	0.671	2.01	BMa18	

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Begonia tenera	F N Hepper	4508	SL	H	K	MBeg12		Ginigathena to Kitulgala, Kegalle District, Sabaragamuwa Province	26/06/1972	*Begonia_tenera_MBeg12*	WGS	0.375	1.38	MBeg12	
Begonia malabarica			IN	F	K	KLBM	1999-3378 GLGO			*Begonia_fallax_KLBM*	WGS	3.845		KLBM	
Begonia hydrophila	Madhavi Sreenath	MASR033	IN	SD		MSF13		Mukkali, Bhavani Range, Silent Valley	19/08/2022	*Begonia_hydrophila_MSF13*	WGS	1.37	2.19	MSF13	
Begonia dipetala	Madhavi Sreenath	MASR040A	IN	SD		MSF14		Bhavani Range, Silent Valley National Park, Karuvar	23/08/2022	*Begonia_dipetala_MSF14*	WGS	0.976	2.27	MSF14	
Begonia anaimalaiensis	Madhavi Sreenath	MASR036B	IN	SD		MSF20		Mukkali, Bhavani Range, Silent Valley	22/08/2022	*Begonia_anaimalaiensis_MSF20*	WGS	1.17	1.8	MSF20	
Begonia phrixophylla	Nikhil Krishna and Sooraj	153681	IN	SD	C	CUBG6		Lodwick point		*Begonia_phrixophylla_CUBG6*	WGS	1.04	1.9	CUBG6	
Begonia trichocarpa	Amrutha and Jeomol	153682	IN	SD	C	CUBG7		Thillari		*Begonia_trichocarpa_CUBG7*	WGS	3.315	1.94	CUBG7	
Begonia handibadaganathensis	Nikhil Krishna and AK Pradeep	168432	IN	SD	C	CUBG8		Handibadaganath		*Begonia_handibadaganathensis_CUBG8*	WGS	4.15	2.08	CUBG8	
							Chloranthaceae								
Chloranthus spicatus	Robert Wight		IN	H	E	MChl02	E00179370	Peninsular India Orientalis		MChl02	WGS	8.245	1.39	MChl02	
Sarcandra grandifolia	Robert Wight	878	IN	H	E	MSar01	E00317628	Courtallam	August 1835	*Sarcandra_grandifolia_MSar01*	LP	10.34	1.4	MSar01	
							Ebenaceae								
Diospyros candolleana	C J Saldanha	16859	IN	H	E	MDio01	E00850302	Vanagur Hassan District	April 25 1970	MDio01	WGS	0.411	2.05	MDio01	
Diospyros neilgherrensis	Robert Wight		IN	H	E	MDio05	E00850310	Peninsular India Orientalis		MDio05	WGS	1.32	2.11	MDio05	
Diospyros nigrescens	C J Saldanha, T P Ramamoorthy	HFP 420	IN	H	E	MDio07	E00850311	Kempuhole Hassan District	August 5 1970	MDio07	WGS	1.009	1.44	MDio07	
Diospyros orixensis	Robert Wight	475/2695	IN	H	E	MDio08	E00850312	Courtallam	August 1835	MDio08	WGS	4.795	1.39	MDio08	

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Diospyros humilis	Robert Wight	475	IN	H	E	MDio12	E00850306	Courtallam	August 1835	MDio12	WGS	1.323	1.09	MDio12	
Diospyros microphylla	W A Talbot	375	IN	H	E	MDio13	E00850305	Yellapora, North Canara	March 10 1883	MDio13	WGS	1.439	1.44	MDio13	
Diospyros sylvatica	Madhavi Sreenath	MASR094	IN	SD		MSF49		Bengaluru, Karnataka	31-Aug-22	MSF49	WGS	7.62	2.17	MSF49	
Diospyros ferrea	Robert Wight	579	IN	H	E	MDio02	E00850304	Quilon (Kollam)	June 1836	*Diospyros_ferrea_MDio02*	LP	22.45	2.06	MDio02	
Diospyros ebeneum	Robert Wight	472	IN	H	E	MDio03	E00850303	Courtallam	March 1835	*Diospyros_ebeneum_MDio03*	LP	9.54	2.04	MDio03	
Diospyros pruriens	T P Ramamoorthy	HFP 1535	IN	H	E	MDio04	E00850313	Kempu hole Shiradi Ghat Hassan District	April 13 1971	*Diospyros_pruriens_MDio04*	WGS	0.66	0.97	MDio04	
Diospyros montana	C J Saldanha	15446	IN	H	E	MDio06	E00850309	Hebbsale on road to Hasbal	October 29 1969	*Diospyros_montana_MDio06*	WGS	1.189	1.47	MDio06	
Diospyros malabarica	Robert Wight	2143	IN	H	E	MDio09	E00850307	Quilon (Kollam)	October 1835/1837	*Diospyros_malabarica_MDio09*	WGS	1.315	2.28	MDio09	
Diospyros melanoxylon	Meebold	9300	IN	H	E	MDio10	E00850308	Kimmsi Maisor (Mysore District)	1908 October	*Diospyros_melanoxylon_MDio10*	LP	13.6	1.99	MDio10	
Diospyros sylvatica	Kostermans	25823	IN	H	E	MDio11	E00850552	Anamalais Kariay Sholas	October 29 1974	*Diospyros_sylvatica_MDio11*	WGS	0.519	1.88	MDio11	
Diospyros geminata	Worboys, S.J.	1348	AU		K	6364-JK-3_001_S1_L005		Australia		*Diospyros_geminata_NM*					Collaboration
Diospyros australis	Frod, A.	2104	AU		K	6364-JK-3_003_S1_L005		Australia		*Diospyros_australis_NM*					Collaboration
Diospyros humilis	Stuart, S.A.	789	AU		K	6364-JK-3_011_S1_L005		Australia		*Diospyros_humilis_NM*					Collaboration
Diospyros defectrix	Beusekom	2079	CA		K	6364-JK-3_020_S1_L005		Thailand		*Diospyros_defectrix_NM*					Collaboration
Diospyros hebecarpa	Fazang, K.M.; et al.	LAE 89113	NG		K	6364-JK-3_025_S1_L005		New Guinea/Papua Newguinea		*Diospyros_hebecarpa_NM*					Collaboration
Diospyros lotus	Meeprom	184	EA		K	6364-JK-4_001_S1_L005		Cultivated in UK (Native to East Asia)		*Diospyros_lotus_NM*					Collaboration
Diospyros mollis	Meeprom	100	CA		K	6364-JK-4_002_S1_L005		Thailand		*Diospyros_mollis_NM*					Collaboration
Diospyros kerrii	Meeprom	172	CA		K	6364-JK-4_010_S1_L005		Thailand		*Diospyros_kerrii_NM*					Collaboration
Diospyros hayatae	Meeprom	149B	CA		K	6364-JK-4_016_S1_L005		Vietnam		*Diospyros_hayatae_NM*					Collaboration
Diospyros siamensis	Meeprom	157	CA		K	6364-JK-4_017_S1_L005		Thailand		*Diospyros_siamensis_NM*					Collaboration

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Diospyros variegata	Meeprom	167	CA		K	6364-JK-4_018_S1_L005		Thailand		*Diospyros_variegata_NM*					Collaboration
Diospyros gracilis	Meeprom	159	CA		K	6364-JK-4_020_S1_L005		Thailand		*Diospyros_gracilis_NM*					Collaboration
Diospyros glandulosa	Meeprom	163	CA		K	6364-JK-4_023_S1_L005		Thailand		*Diospyros_glandulosa_NM*					Collaboration
Diospyros ferrea	Meeprom	166	CA		K	6364-JK-4_041_S1_L005		Thailand		*Diospyros_ferrea_NM*					Collaboration
Diospyros neuvoguineensis	Kanis, A.	1048	NG		K	7533-JK-2_019_S1_L005		New Guinea/Papua Newguinea		*Diospyros_neuvoguineensis_NM*					Collaboration
Diospyros tricolor	Bayor	WP078	WA		K	7533-JK-2_021_S1_L005		Ghana		*Diospyros_tricolor_NM*					Collaboration
Dipterocarpaceae															
Hopea sp	Madhavi Sreenath	MASR086	IN	SD		MSF46		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Hopea_sp_MSF46*	WGS	3.14	2.13	MSF46	Sample was misidentified at collection
Lauraceae															
Actinodaphne angustifolia	Meebold	9590	IN	H	E	MAct08	E00068676	Gersoppa (Jog) Falls Maisor	April or October 1908	MAct08	LP	5.8	2.09	MAct08	
Actinodaphne malabarica	F M Jarrett, C J Saldanha and T P Ramamoorthy	812	IN	H	E	MAct09	E00068692	Near Hullahali	October 6 1970	MAct09	WGS	1.125	1.97	MAct09	
Cinnamomum wightii	H F Cleghorn and sq M D		IN	H	E	MCin15	E00850290	Nilgiri Hills	1855	MCin15	LP	4.305	1.93	MCin15	
Cinnamomum sulphuratum	T P Ramamoorthy	HFP 1558	IN	H	E	MCin16	E00850289	Banagere	April 14 1971	MCin16	WGS	0.079	1.75	MCin16	
Litsea floribunda	T P Ramamoorthy	1765	IN	H	E	MLit05	E00850296	Bannuhalla, Hassan District	June 5 1971	MLit05	WGS	0.178	1.7	MLit05	
Litsea laevigata	Robert Wight	712	IN	H	E	MLit18	E00850297	Courtallam	August 1835	MLit18	LP	7.12	2.02	MLit18	
Actinodaphne sp	Kostermans	25810	IN	H	E	MAct11	E00068715	Between Godalur and Pandalur, Nilgiris	October 25 1974	MAct11	WGS	0.164	2.18	MAct11	
Apollonias arnottii	Robert Wight	710	IN	H	E	MApo20	E00850292	Courtallam	August 1835	MApo20	WGS	0.443	0.95	MApo20	
Neolitsea scrobiculata	Kostermans	25822	IN	H	E	MNeo02	E00850300	Anaimalais, Kariay Sholas	October 29 1974	MNeo02	WGS	0.533	4.61	MNeo02	
Cinnamomum zeylanicum			IN	H	E	MCin17	E00850291	Avalanche	March 26 1889	MCin17	WGS	2.6	1.78	MCin17	

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Neolitsea	Madhavi Sreenath	MASR047	IN	SD		MSF39		Bhavani Range, Silent Valley National Park	23/08/2022	MSF39	WGS	2.1	2.24	MSF39	
Neolitsea oblonga	Robert Wight	856	IN	H	E	MNeo01	E00850299	Courtallam	February 1836	*Neolitsea_oblonga_MNeo01*	LP	4.295	1.95	MNeo01	
Actinodaphne hookeri			IN	H	E	MAct10	E00850286	Mahabaleshwar	Aprill 1853	*Actinodaphne_hookeri_MAct10*	WGS	1.73	1.74	MAct10	
Alseodaphne semicarpifolia		858, 143/18	IN	H	E	MAls12	E00850285	Courtallam	1836	*Alseodaphne_semicarpifolia_MAls12*	WGS	1.54	1.4	MAls12	
Cinnamomum iners		718	IN	H	E	MCin13	E00850287	Courtallam	August 1835	*Cinnamomum_iners_MCin13*	WGS	1.064	3.17	MCin13	
Cinnamomum macrocarpum	Kostermans	24532	IN	H	E	MCin14	E00850288	Nilgiris near Pykara, Shola forest on laterite	April 3 1973	*Cinnamomum_macrocarpum_MCin14*	WGS	2.95	2.26	MCin14	
Litsea coriacea	Robert Wight	881	IN	H	E	MLit04	E00850293	Quilon (Kollam)	October 1835	*Litsea_coriacea_MLit04*	WGS	2.55	1.93	MLit04	
Litsea glabrata	Meebold	9132	IN	H	E	MLit06	E00850295	Kuhully, Bababudan Hills	1907 November	*Litsea_glabrata_MLit06*	LP	23.05	1.92	MLit06	
Litsea deccanensis	C J Saldanha	17936	IN	H	E	MLit07	E00850294	Achihalli, Hassan District	September 16 1969	*Litsea_deccanensis_MLit07*	WGS	0.932	3.3	MLit07	
Litsea lingustrina	Robert Wight	763	IN	H	E	MLit19	E00850298	Courtallam	September 1835	*Litsea_lingustrina_MLit19*	WGS	1.555	1.64	MLit19	
Neolitsea zeylanica	Robert Wight	2225/2804	IN	H	E	MNeo03	E00850301	Pulney Mountains	September 1835	*Neolitsea_zeylanica_MNeo03*	WGS	2.37	1.9	MNeo03	
Cinnamomum malabatrum	Madhavi Sreenath	MASR011	IN	SD		MSF4		Suntikoppa, Madikeri	16/08/2022	*Cinnamomum_sp_MSF4*	WGS	3.6	2.17	MSF4	
Cinnamomum sp	Madhavi Sreenath	MASR022	IN	SD		MSF6		Somwarpet, Madikeri	18/08/2022	*Cinnamomum_sp_MSF6*	WGS	15.2	2.14	MSF6	
Cinnamomum sp	Madhavi Sreenath	MASR077	IN	SD		MSF26		Muthanga Wildlife Sanctuary, Wayanad	03/09/2022	*Cinnamomum_sp_MSF26*	WGS	8.5	2.2	MSF26	
Cinnamomum malabatrum	Madhavi Sreenath	MASR056	IN	SD		MSF31		Kottebetta, Madhapura Range, Somwarpet	01/09/2022	*Cinnamomum_malabatrum_MSF31*	WGS	5.06	2.07	MSF31	

Taxon Name	Collector Name(s)	Collecto Number	Country	Material Type	Herbarium	User DNA ID	Herbarium Barcode	Location	Collection Date	Sample name in phylogeny	Lab Protocol	Qubit ng/µL	Nano Drop ng/µL		Notes
Cinnamomum zeylanicum	Madhavi Sreenath	MASR055	IN	SD		MSF32		Kottebetta, Madhapura Range, Somwarpet	01/09/2022	*Cinnamomum_sp_MSF32*	WGS	7.36	2.16	MSF32	
Persea macarantha	Madhavi Sreenath	MASR092	IN	SD		MSF47			03/09/2022	*Persea_macarantha_MSF47*	WGS	1.1	2.26	MSF47	
Litsea sp	Madhavi Sreenath	MASR041	IN	SD		MSF24		Bhavani Range, Silent Valley National Park	23/08/2022	*Litsea_sp_MSF24*	WGS	1.44	2.15	MSF24	
Sapotaceae															
Isonandra stocksii	T P Ramamoorthy		IN	H	E	MSap02	E00325123	Hassan District	April 14 1971	MSap02	WGS	0.05	1.41	MSap02	Extracted twice
Madhuca neriifolia	Captain R H Beddome		IN	H	E	MSap05	E00277964	Anamallai Hills	1859	MSap05	WGS	1.29	2.12	MSap05	Extracted twice
Madhuca diplostemon	Robert Wight	583	IN	H	E	MSap06	E00277959	Quilon (Kollam)	December 1835	MSap06	LP	3.47	1.77	MSap06	Extracted twice
Mimusops elengi	Robert Wight	586	IN	H	E	MSap07	E00277903	Quilon (Kollam)	September 1836	MSap07	WGS	1.96	1.82	MSap07	Extracted twice
Palaquim ellipticum	Dr Drew		IN	H	E	MSap08	E00277819	Wynaad (Wayanad) Gutta Purcha	1857	MSap08	WGS	0.485	1.01	MSap08	Extracted twice
Madhuca longifolia	Madhavi Sreenath	MASR095	IN	SD		MSF50		Karnataka	31-Aug-22	MSF50	WGS	1.45	2.19	MSF50	
Isonandra villosa	Robert Wight	2147	IN	H	E	MSap01	E00179153	Peninsular India Orientalis	1837	*Isonandra_villosa_MSap01*	LP	5.15	2.17	MSap01	Extracted twice
Isonandra perottetiana			IN	H	E	MSap03	E00325138	Sispara Ghat	January 13 1889	*Isonandra_perottetianan_MSap03*	LP	4.01	1.92	MSap03	Extracted twice
Isonandra lanceolata	Robert Wight	482	IN	H	E	MSap04	E00179150	Courtallam	August 1835	*Isonandra_lanceolata_MSap04*	WGS	1.735	1.79	MSap04	Extracted twice
Madhuca sp	Madhavi Sreenath	MASR057	IN	SD		MSF45		Madapura Range, Somwarpet, Madikeri District	01-Sep-22	*Madhuca_sp_MSF45*	WGS	4.18	2.19	MSF45	
Mimusops elengi	Madhavi Sreenath	MASR093	IN	SD		MSF48		Karnataka	31-Aug-22	*Mimusops_elengi_MSF48*	WGS	9.28	2.21	MSF48	
Zingiberaceae															
Boesenbergia pulcherrima	C J Saldanha	14438	IN	H	E	MBoe06	E00389693	Kempuhole Shiradi Ghat	August 7 1969	MBoe06	WGS	1.67	1.56	MBoe06	
Globba sessiflora	Robert Wight		IN	H	E	MGob07	E00097423	Peninsular India Orientalis		MGob07	WGS	1.419	2.3	MGob07	

Taxon Name	Collector Name(s)	Collecto Number	Country	Material Type	Herbarium	User DNA ID	Herbarium Barcode	Location	Collection Date	Sample name in phylogeny	Lab Protocol	Qubit ng/µL	Nano Drop ng/µL		Notes
Heydychium spicatum	H F Cleghorn and sq M D		IN	H	E	MHey09	E00531010	Ootacamund	1850	MHey09	WGS	2.88	2.06	MHey09	
Heydychium sp	K M Matthew, M Charles and N Rajendren	46992	IN	H	E	MHey10	E00031899	Anna Pulney Hills, Between Perumalmalai and Vedakavunchi	September 23 1986	MHey10	WGS	0.179	1.7	MHey10	
Heydychium coronarium	K M Matthew	14818	IN	H	E	MHey11	E00211114	Dolphin's Hole Kodaikanal	August 16 1975	MHey11	LP	5.025	2	MHey11	
Zingiber sp	Robert Wight	937	IN	H	E	MZin01	E00389858	Courtallam	September 1835	MZin01	WGS	6.915	1.95	MZin01	
Zingiber sp	Robert Wight	1060	IN	H	E	MZin02	E00389854	Peninsular India Orientalis	June 1835	MZin02	WGS	2.56	2	MZin02	
Zingiber neesanum	C J Saldanha	17937	IN	H	E	MZin03	E00389839	Achihalli, Hassan District	October 16 1969	MZin03	WGS	0.2	2.59	MZin03	
Zingiber officinale	H F Cleghorn and sq M D		IN	H	E	MZin04	E00389845	Anamally	1859	MZin04	WGS	1.01	2.36	MZin04	
Globba marantina	Robert Wight	1072	IN	H	E	MGob08	E00095793	Malabar	June 1836	*Globba_marantina_MGob08*	WGS	1.735	1.67	MGob08	
Heydychium flavescens	Robert Wight	3050	IN	H	E	MHey12	E00507925	Pulney Mountains	September 1836	*Heydychium_flavescens_MHey12*	WGS	1.325	1.85	MHey12	
Zingiber cylandricum	Meebold	9085	IN	H	E	MZin05	E00389824	Castle Rock, Concan (Konkan)	1908 October	*Zingiber_cylandricum_MZin05*	WGS	0.947	1.91	MZin05	
Heydychium	Madhavi Sreenath	MASR003	IN	SD		MSF2		Madikeri, Coorg	08-Aug-22	*Heydychium_villosum_MSF2*	WGS	8.54	2.15	MSF2	
Cucurma sp	Madhavi Sreenath	MASR024	IN	SD		MSF7		Shanthahalli, Devarkadu, Somwarpet	18-Aug-22	*Cucurma_sp_MSF7*	WGS	18.08	2.15	MSF7	
Globba sessiliflora	Madhavi Sreenath	MASR039	IN	SD		MSF21		Mannarkkad, Bhavani Range, Silent Valley National Park	22-Aug-22	*Globba_sessiliflora_MSF21*	WGS	10.8	2.16	MSF21	
Amomum sp	Madhavi Sreenath	MASR025	IN	SD		MSF23		Shanthahalli, Devarkadu, Somwarpet	18-Aug-22	*Amomum_sp_MSF23*	WGS	20.4	2.16	MSF23	

Taxon Name	Collector Name(s)	Collecto Number	Country	Material Type	Herbarium	User DNA ID	Herbarium Barcode	Location	Collection Date	Sample name in phylogeny	Lab Protocol	Qubit ng/µL	Nano Drop ng/µL		Notes
Alpinia sp	Madhavi Sreenath	MASR044	IN	SD		MSF25		Panthanthode, Bhavani Range, Silent Valley National Park	23-Aug-22	*Alpinia_sp_MSF25*	WGS	4.66	2.22	MSF25	
Elettaria cardamomum	Madhavi Sreenath	MASR058	IN	SD		MSF29		Sirangalli, On the way to Kooti Betta, Madapura Range, Somwarpet	01-Sep-22	*Elettaria_cardamomum_MSF29*	WGS	8.22	2	MSF29	
Zingiber officinale	Madhavi Sreenath	MASR089	IN	SD		MSF34		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Zingiber_officinale_MSF34*	WGS	3.46	2.14	MSF34	
Zingiber sp	Madhavi Sreenath	MASR072	IN	SD		MSF35		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Zingiber_nimmonii_MSF35*	WGS	4.38	2.13	MSF35	
Cucurma sp	Madhavi Sreenath	MASR091	IN	SD		MSF36		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Cucurma_sp_MSF36*	WGS	18.1	2.11	MSF36	
Zingiber sp	Madhavi Sreenath	MASR059	IN	SD		MSF38		On the way to Kooti Betta, Madhapura Range, Somwarpet	01-Sep-22	*Zingiber_sp_MSF38*	WGS	28.8	2.14	MSF38	
Globba sp	Madhavi Sreenath	MASR087	IN	SD		MSF40		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Globba_bulbifera_MSF40*	WGS	16.4	2.07	MSF40	
Zingiber sp	Madhavi Sreenath	MASR088	IN	SD		MSF42		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Zingiber_sp_MSF42*	WGS	45.6	2.12	MSF42	
Alpinia sp	Madhavi Sreenath	MASR042	IN	SD		MSF43		Panthanthode, Bhavani Range, Silent Valley National Park	23-Aug-22	*Alpinia_sp_MSF43*	WGS	6.42	2.13	MSF43	
Cucurma sp	Madhavi Sreenath	MASR090	IN	SD		MSF44		Muthanga Wildlife Sanctuary, Wayanad	03-Sep-22	*Cucurma_sp_MSF44*	WGS	17.36	2.19	MSF44	

Table A.1: Specimen list. Taxa highlighted in pink are not in the final phylogenies due to a failure to sequence, lack of viable data or being replicates. Codes: IN – India, SL – Sri Lanka, CA – Continental Asia, AU – Australia, NG – New Guinea, WA – West Africa, H – Herbarium, F – Fresh, SD – Silica Dried, E – RBGE, K – Kew, C – CUBG, WGS – Library preparation and Whole Genome Sequencing with a company, LP - In house library preparation prior to WGS with a company.

A.2 Checklist of WG Flora

https://doi.org/10.5281/zenodo.8400056

A.3 Wet Lab

A.3.1 Altered Qiagen DNeasy Extraction Protocol

1. To a mixer mill tube add approximately 5g of leaf material and two mixer mill beads. Make three additional replicates for each sample. Store at -20ºC overnight (minimum an hour). Grind to a fine powder using a Thermo Fischer MM 400 Mixer Mill for two one-minute rounds. Add additional time based on necessity. Alternatively grind using liquid nitrogen and mortar and pestle.
2. Place DNeasy Buffer AP1 in 65ºC water bath to dissolve precipitate.
3. Add 800µL of Buffer AP1 to each tube of ground material from step one.
4. Incubate the tubes for an hour at 65ºC in a Thermomixer set to 800rpm. Tubes must be agitated constantly.
5. Remove samples from the thermomixer and add 260µL of DNeasy Buffer P3 to the lysate mix and incubate for 30 minutes at -20ºC.
6. Centrifuge the lysate for 5 minutes at 13,000 rpm
7. Pipette the lysate mixture into the lilac coloured QIAshredder Mini spin column with 2ml collection tubes and spin for 2 minutes at 13,000 rpm.
8. Transfer the flow through fraction from step 7 into a 15ml falcon tube without disturbing the cell debris pellet at the bottom. Set aside mixer mill tubes with debris to remove and clean mixer mill beads.
9. Combine the replicate tubes for each sample in the falcon tubes.
10. Add 1.5 times the volume of the flow-through of DNeasy Buffer AW1 to the lysate and mix by pipetting. You should be able to see the precipitate. Using the same pipette transfer 650µL of the mixture including the precipitate into the white DNeasy mini spin columns with a 2ml collection tube.
11. Centrifuge for 1 minute at 8000 rpm and discard flow-through in the appropriate waste bottle. Re-use the collection tube from step 10.
12. Repeat steps 10 and 11 until there is no lysate mixture remaining in the falcon tubes. Your DNA will be on the white filter at the bottom of the spin column. Do not discard the columns.
13. Place the columns in a new 2ml collection tube, add 500µL of Buffer AW2 and centrifuge for 1 minute at 8000 rpm. Discard the flow-through in the appropriate waste bottle and reuse the collection tubes for the next step.
14. Add another 500µL Buffer of AW2 to the white Buffer mini spin column and spin for one minute at 8000 rpm. Discard the flow-through and centrifuge again to catch any remaining liquid in the spin column. Discard flow-through and the collection tube.
15. Transfer the spin column to a new 1.5ml micro-centrifuge collection tube and apply 35µL of 0.1xTE solution directly onto the filter. Incubate for 5 minutes at room temperature and then spin one minute at 8000 rpm to elute.

16. To the same spin column with the same collection tube from step 15 add another 30µL of 0.1xTE solution. Incubate for 5 minutes at room temperature and then spin for one minute at 8000 rpm to elute.
17. The 65µL of DNA can now be stored at -20ºC.

A.4 Bioinformatics

A.4.1 Plastid Region Miner Script

Based on Legacy Miner Pipeline (unpublished, Wilson 2020).

Script

```
#!/bin/bash
#SBATCH --job-name=PRM
#SBATCH --cpus-per-task=16
#SBATCH --mem=32G
#SBATCH --output=PRM.%j.out
#SBATCH --error=PRM.%j.err
#SBATCH --partition=long

# ***********************************
#    Plastid Region Miner (PRM) *
#          Madhavi Sreenath          *
# ***********************************

#Complete path and set configuration for selected location
	echo -e "\nPlastid Region Miner is running on Gruffalo...\n"

# Load settings from settingsmal.cfg (stored in home directory)
. ~/path/to/directory/settings.cfg
cat ~/path/to/directory/settings.cfg

#Make and enter a working directory for the job
mkdir ~/path/to/directory/$SLURM_JOBID
cd ~/path/to/directory/$SLURM_JOBID

# Copy files from data repository
cp $data/*fq.gz .
cp $Ref .
cp $data/SamplesFileNames.txt .

#Add LF at the end of last line in SamplesFileNames.txt if missing
sed -i.bak '$a\' SamplesFileNames.txt

#Delete empty lines from SamplesFileNames.txt (if any)
sed -i.bak2 '/^$/d' SamplesFileNames.txt

#Build bowtie index
bowtie2-build $Ref RefIndex

if [[ $trimmed =~ "yes" ]]; then
```

```
    echo -e "\nReads trimmed using trimmomatic..."
    numberfiles=$(cat SamplesFileNames.txt | wc -l)
    calculating=0
    for file in $(cat SamplesFileNames.txt) #A loop to process all samples as specified in
SamplesFileNames.txt
    do calculating=$((calculating + 1))
        echo -e "\nProcessing sample $file ($calculating out of $numberfiles)"
        #Trim raw reads
            java -jar /path/to/package/trimmomatic-0.39-1/share/trimmomatic-0.39-
1/trimmomatic.jar PE -phred33 ${file}_R1.fq.gz ${file}_R2.fq.gz ${file}_forward_paired.fq.gz
${file}_forward_unpaired.fq.gz ${file}_reverse_paired.fq.gz ${file}_reverse_unpaired.fq.gz
ILLUMINACLIP:$adapterfile:2:30:10 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15
MINLEN:36 >Trimmomatic.log 2>&1
       #Map raw reads to reference using bowtie2
            bowtie2 --local --score-min G,10,8 -x RefIndex -1 ${file}_forward_paired.fq.gz
-2 ${file}_reverse_paired.fq.gz  -U
${file}_forward_unpaired.fq.gz,${file}_reverse_unpaired.fq.gz -S Trimmed_${file}_to_ref.sam
2>Trimmed_${file}_bowtie_out
        #Identify how many of these reads were mapped
            head Trimmed_${file}_bowtie_out
          #Check the @s in header
        head Trimmed_${file}_to_ref.sam
            #Remove unmapped reads to reduce size of the file
        samtools view -h -F 4 -b Trimmed_${file}_to_ref.sam >
MappedTrimmed_${file}.bam
        #Sort the bam file
            samtools sort MappedTrimmed_${file}.bam > Sorted_${file}.bam
        #Index the bam file
            samtools index Sorted_${file}.bam Sorted_${file}.bai
        echo "Remove soft clip annotations with python..."
        #Change CIGAR string annotations of soft clipped reads to matches/mismatches
and recalculate CIGAR string qualifier numbers
        python $Soft Sorted_${file}.bam


    done

else
       echo -e "\nReads not trimmed..."
    numberfiles=$(cat SamplesFileNames.txt | wc -l) #A loop to process all samples as
specified in SamplesFileNames.txt
    calculating=0
    for file in $(cat SamplesFileNames.txt)
    do calculating=$((calculating + 1))
        echo -e "\nProcessing sample $file ($calculating out of $numberfiles)"
            #Map raw reads to reference using bowtie2
            bowtie2 --local --score-min G,10,8 -x RefIndex -1 ${file}_R1.fq.gz  -2
${file}_R2.fq.gz  -S Bowtied_${file}.sam 2>Bowtied_${file}_bowtie_out
        #Identify how many of these reads were mapped
            head Bowtied_${file}_bowtie_out
            #Check the @s in header
        head Bowtied_${file}.sam
```

```
                #Remove unmapped reads to reduce size of the file
            samtools view -h -F 4 -b Bowtied_${file}.sam > MappedBowtied_${file}.bam
                #Sort the bam file
            samtools sort MappedBowtied_${file}.bam > Sorted_${file}.bam
                #Index the bam file
            samtools index Sorted_${file}.bam Sorted_${file}.bai
            echo "Remove soft clip annotations with python..."
                #Change CIGAR string annotations of soft clipped reads to
matches/mismatches and recalculate CIGAR string qualifier numbers
            python $Soft Sorted_${file}.bam

      done
fi

#Remove raw files from working directory
rm *.fq.gz

#Rename headings inside fasta files to include name of the file
for i in *.fasta
          do n="${i%.fasta}"
          sed -i.bak "s/>[^_]\+/>$n/" $i
      sed -i.bak "s/_cns <unknown description>//" $i
done

#Make directory for no soft bam files
mkdir ~/path/to/directory

#Copy all no soft bam files to another directory
cp *_nosoft.bam ~/path/to/directory

echo "\nMove to Geneious pipeline ....n\"

echo "\nPlastid Region Miner for Whole Genome Sequencing part one is complete...n\"
**********************************************************************************************
```

Settings File

```
Setting the stage! - All the world is a stage!!

#Location of raw data
data=~/path/to/data

#Location of reference file
Ref=~/path/to/reference/file

#Location of soft2match python script
Soft=~/path/to/script/soft2match.py

#trim reads prior to mapping (using trimmomatic)'=yes'  or process reads without
trimming '=no'
```

```
trimmed=no
*********************************************************************************************
```

A.4.2 Concatenation Script

Script

```
#!/bin/bash
#SBATCH --job-name=CW
#SBATCH --cpus-per-task=4
#SBATCH --mem=8G
#SBATCH --output=CW.%j.out
#SBATCH --error=CW.%j.err
#SBATCH --partition=medium



# Concatenation of mapped and assembled genes fastas #
#                    Madhavi Sreenath                 #


#Load settings
. ~/path/to/directory/settings2.cfg
cat ~/path/to/directory/settings2.cfg

#Copy fastas to current directory
cp $data/*.fasta .

#Make a directory for used files
mkdir Processed

#Build multifasta for each loci and move single seq fastas
cat *_loci1.fasta > loci1.fas
cat *_loci2.fasta > loci2.fas
cat *_loci3.fasta > loci3.fas

#Tidy directory
mv *.fasta Processed

#Copy legacy daata from Legacy
cp $legacy/*.fasta .

#Combine the legacy data and newly generated data
cat loci1.fas New_Mega_loci1.fasta > loci1.fasta
cat loci2.fas New_Mega_loci2.fasta > loci2.fasta
cat loci3.fas New_Mega_loci3.fasta > loci3.fasta

#Tidy directory
```

```
mv *.fas New_Mega_* Processed

#Use MAFFT to align sequences in each loci specific multifasta
cp ~/path/to/directory/loci .
for file in $(cat loci)
	do
	mafft ${file} > aligned_${file}
done

echo "done"

# remove loci tags from headers so amas can match up samples
sed 's/_loci1//g' aligned_loci1.fasta > clean_aligned_loci1.fas
sed 's/_loci2//g' aligned_loci2.fasta > clean_aligned_loci2.fas
sed 's/_loci3//g' aligned_loci3.fasta > clean_aligned_loci3.fas

#Make working directory for AMAS, move clean alignments to it and move into it
mkdir AMAS
cp clean_aligned_* AMAS/
cd AMAS

#Concatenate gene alignments using AMAS. - output file in fasta format; Note if
there is a specific order of genes for concatenation this order has to be put in place of
*fas
python $AMAS concat -f fasta -d dna -i *fas -u fasta

cp concatenated.out concat.fasta

echo "concatenated gene alignment written to concatenated.fasta"

#Remove "." from sample names
sed 's/.//g' concat.fasta

#Delete empty lines
sed '/^$/d' concat.fasta

#Removes line breaks from fasta file
awk '!/^>/ { printf "%s", $0; n = "\n" } /^>/ { print n $0; n = "" } END { printf "%s", n
}' concat.fasta > alignment.fasta

#Replace newline with ' ' if line starts with '>' (i.e., merge headers with data into
single line separated by space)
sed '/^>/{N; s/\n/ /;}' alignment.fasta
```

****

Settings file

```
#!/bin/bash
```

```
#SBATCH --job-name=CW
#SBATCH --cpus-per-task=4
#SBATCH --mem=8G
#SBATCH --output=CW.%j.out
#SBATCH --error=CW.%j.err
#SBATCH --partition=medium


#Concatenation of mapped and assembled gene sequences#
#                          Madhavi Sreenath         #

#Path to new data
data=~/path/to/new/data

# path to existing data - multifastas for each loci containging existing data, e.g.
sanger. filename must end '_loci.fasta'
legacy=~/path/to/legacy/data

# make loci list file
printf 'loci1.fasta\nloci2.fasta\nloci3.fasta' > loci

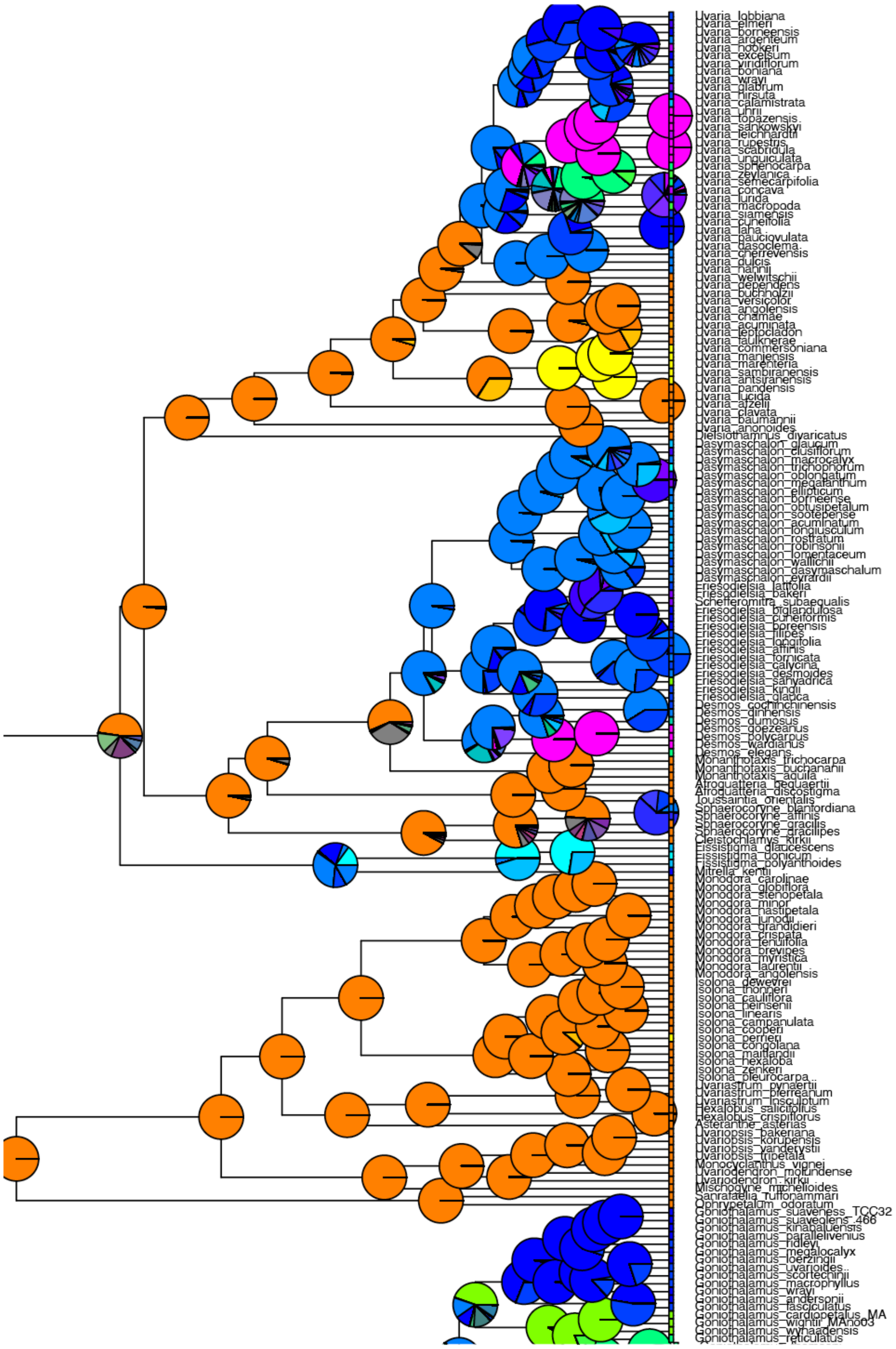
# path to AMAS
AMAS=/path/to/AMAS/amas-1.0-pyh864c0ab_0/site-packages/amas/AMAS.py

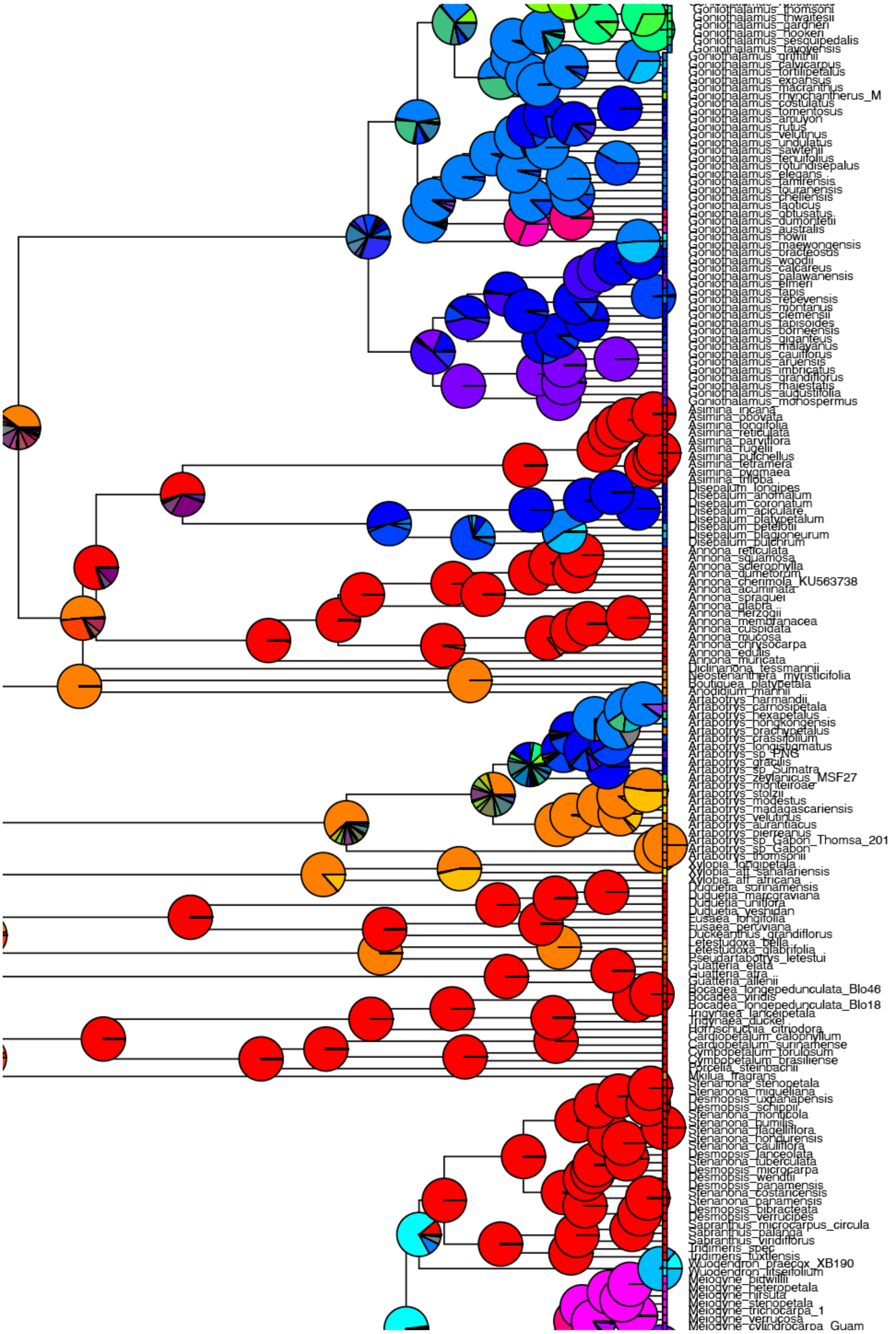
****************************************************************************************************
```

A.5 BioGeoBEARS

A.5.1 *Annonaceae*

DEC+J Reconstruction




Goniothalamus_thomsoni
Goniothalamus_thwaitesii
Goniothalamus_gardneri
Goniothalamus_hookeri
Goniothalamus_sesquipedalis
Goniothalamus_tavoyensis
Goniothalamus_griffithii
Goniothalamus_calvicarpus
Goniothalamus_tortilipetalus
Goniothalamus_expansus
Goniothalamus_macranthus
Goniothalamus_rhynchantherus_M
Goniothalamus_costulatus
Goniothalamus_tomentosus
Goniothalamus_amuyon
Goniothalamus_rufus
Goniothalamus_velutinus
Goniothalamus_undulatus
Goniothalamus_sawtehii
Goniothalamus_tenuifolius
Goniothalamus_rotundisepalus
Goniothalamus_elegans
Goniothalamus_tamirensis
Goniothalamus_touranensis
Goniothalamus_cheliensis
Goniothalamus_laoticus
Goniothalamus_obtusatus
Goniothalamus_dumontetii
Goniothalamus_australis
Goniothalamus_howii
Goniothalamus_maewongensis
Goniothalamus_bracteosus
Goniothalamus_woodii
Goniothalamus_calcareus
Goniothalamus_palawanensis
Goniothalamus_elmeri
Goniothalamus_tapis
Goniothalamus_repevensis
Goniothalamus_montanus
Goniothalamus_clemensii
Goniothalamus_tapisoides
Goniothalamus_borneensis
Goniothalamus_giganteus
Goniothalamus_malayanus
Goniothalamus_cauliflorus
Goniothalamus_aruensis
Goniothalamus_imbricatus
Goniothalamus_grandiflorus
Goniothalamus_majestatis
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Goniothalamus_monospermus
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Asimina_longifolia
Asimina_reticulata
Asimina_parviflora
Asimina_rugelii
Asimina_pulchellus
Asimina_tetramera
Asimina_pygmaea
Asimina_triloba
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Disepalum_anomalum
Disepalum_coronatum
Disepalum_aciculare
Disepalum_platypetalum
Disepalum_petelotii
Disepalum_plagioneurum
Disepalum_pulchrum
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Annona_squamosa
Annona_sclerophylla
Annona_dumetorum
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Annona_spraguei
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Annona_herzogii
Annona_membranacea
Annona_cuspidata
Annona_mucosa
Annona_chrysocarpa
Annona_edulis
Annona_muricata
Diclinanona_tessmannii
Neostenanthera_myristicifolia
Boutiquea_platypetala
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Artabotrys_sp_Sumatra
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Artabotrys_monteiroae
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Artabotrys_madagascariensis
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Artabotrys_aurantiacus
Artabotrys_pierreanus
Artabotrys_sp_Gabon_Thomsa_201
Artabotrys_sp_Gabon
Artabotrys_thomsonii
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Xylopia_aff_africana
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Duguetia_uniflora
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Porcelia_steinbachii
Mkilua_fragrans
Stenanona_stenopetala
Stenanona_migueliana
Desmopsis_uxpanapensis
Desmopsis_schippii
Stenanona_monticola
Stenanona_humilis
Stenanona_flagelliflora
Stenanona_hondurensis
Stenanona_cauliflora
Desmopsis_lanceolata
Stenanona_tuberculata
Desmopsis_microcarpa
Desmopsis_wendtii
Desmopsis_panamensis
Stenanona_costaricensis
Stenanona_panamensis
Desmopsis_bibracteata
Desmopsis_verrucipes
Sapranthus_microcarpus_circula
Sapranthus_palanga
Sapranthus_viridiflorus
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Wuodendron_praecox_XB190
Wuodendron_litseifolium
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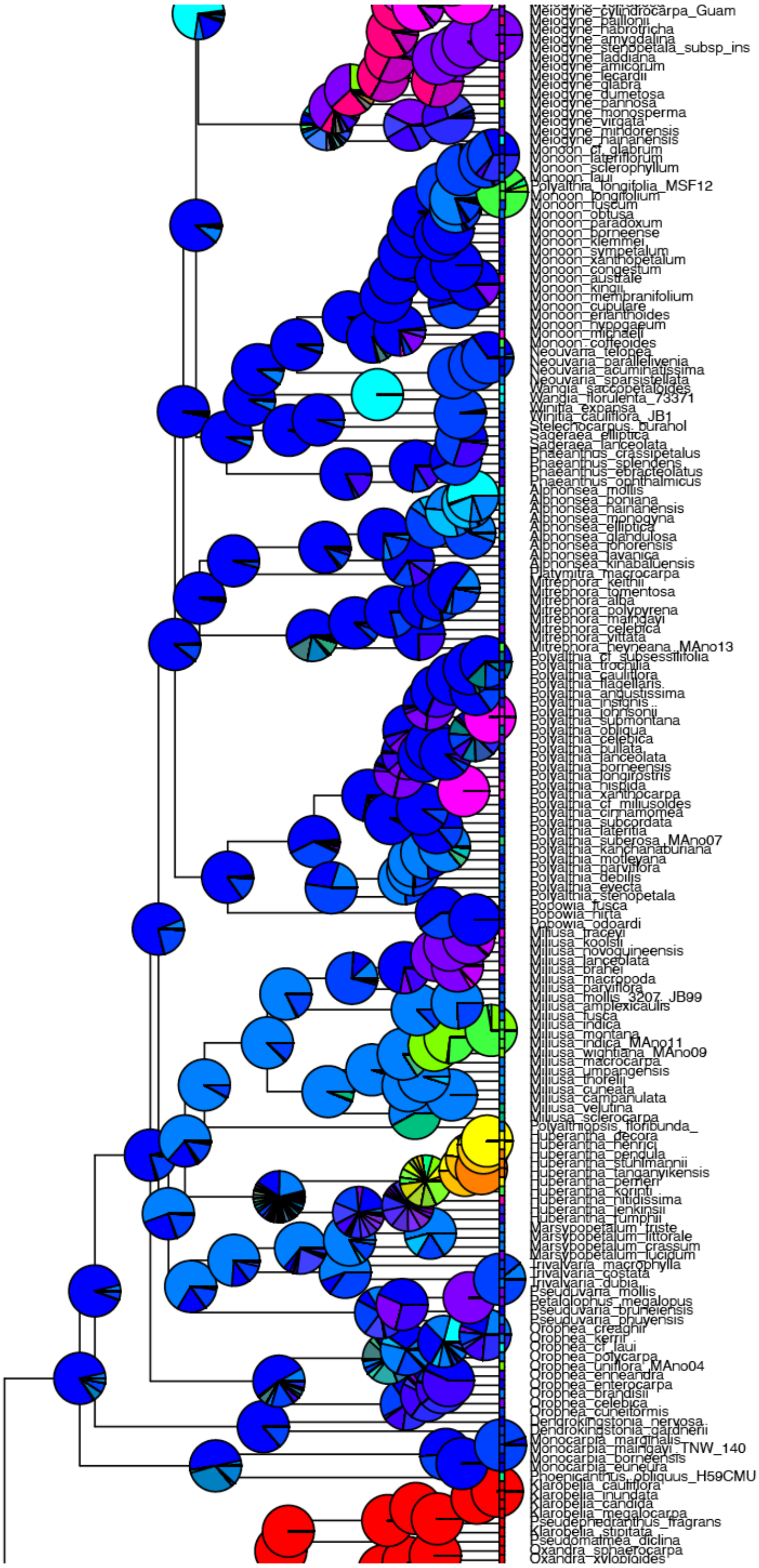
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Monoon_fuscum
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Monoon_xanthopetalum
Monoon_congestum
Monoon_australe
Monoon_kingii
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Miliusa_cuneata
Miliusa_campanulata
Miliusa_velutina
Miliusa_sclerocarpa
Polyalthiopsis_floribunda_
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Huberantha_henrici
Huberantha_pendula
Huberantha_stuhlmannii
Huberantha_tanganyikensis
Huberantha_perrieri
Huberantha_korinti
Huberantha_nitidissima
Huberantha_jenkinsii
Huberantha_rumphii
Marsypopetalum_triste
Marsypopetalum_littorale
Marsypopetalum_crassum
Marsypopetalum_lucidum
Trivalvaria_macrophylla
Trivalvaria_costata
Trivalvaria_dubia
Pseuduvaria_mollis
Petalolophus_megalopus
Pseuduvaria_bruneiensis
Pseuduvaria_phuyensis
Orophea_creaghii
Orophea_kerrii
Orophea_cf_laui
Orophea_polycarpa
Orophea_uniflora_MAno04
Orophea_enneandra
Orophea_enterocarpa
Orophea_brandisii
Orophea_celebica
Orophea_cuneiformis
Dendrokingstonia_nervosa.
Dendrokingstonia_gardnerii
Monocarpia_marginalis
Monocarpia_maingayi_TNW_140
Monocarpia_borneensis
Monocarpia_euneura
Phoenicanthus_obliquus_H59CMU
Klarobelia_cauliflora
Klarobelia_inundata
Klarobelia_candida
Klarobelia_megalocarpa
Pseudephedranthus_fragrans
Klarobelia_stipitata
Pseudomalmea_diclina
Oxandra_sphaerocarpa
Oxandra_xylopioides

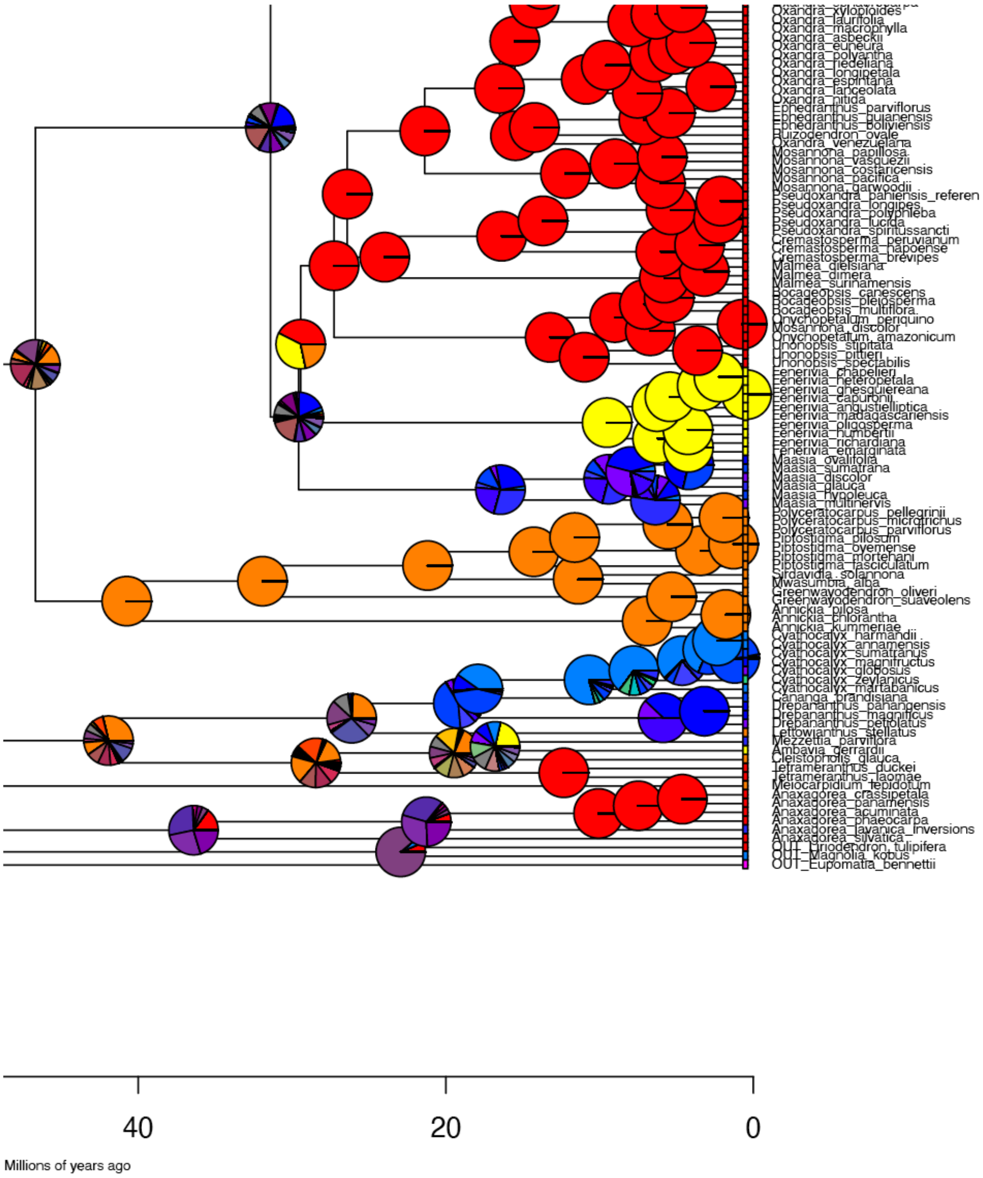

Figure A.1: DEC+J ancestral area reconstruction for the family *Annonaceae.*

Log likelihood Values

Model	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-1484	2	0.0032	1.0e-12	0	2973	2.4e-56
DEC+J	-1444	3	0.0025	1.6e-09	0.0068	2893	4.2e-39
BAYAREALIKE	-1356	3	0.0011	0.013	0.0091	2718	0.50
BAYAREALIKE+J	-1356	3	0.0011	0.013	0.0090	2718	0.50

Table A.2: Log likelihood values for four models of biogeographic analyses run using BioGeoBEARS.

Scored Geography

602 12(A B C D E F G H I J K L)

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OUT_Magnolia_kobus	000000010000
OUT_Liriodendron_tulipifera	100000000000
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Anaxagorea_javanica_inversions	000000011100
Anaxagorea_phaeocarpa	100000000000
Anaxagorea_acuminata	100000000000
Anaxagorea_panamensis	100000000000
Anaxagorea_crassipetala	100000000000
Meiocarpidium_lepidotum	010000000000
Tetrameranthus_laomae	100000000000
Tetrameranthus_duckei	100000000000
Cleistopholis_glauca	010000000000
Ambavia_gerrardii	001000000000
Mezzettia_parviflora	000000011100
Lettowianthus_stellatus	010000000000
Drepananthus_petiolatus	000000000100
Drepananthus_magnificus	000000001000
Drepananthus_pahangensis	000000001000
Cananga_brandisiana	000000011000
Cyathocalyx_martabanicus	000000010000
Cyathocalyx_zeylanicus	000101010000
Cyathocalyx_globosus	000000000100
Cyathocalyx_magnifructus	000000001000
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Annickia_chlorantha	010000000000
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Maasia_glauca	000000011100
Maasia_discolor	000000000100

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Maasia_ovalifolia	000000001000
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Petalolophus_megalopus	000000000100
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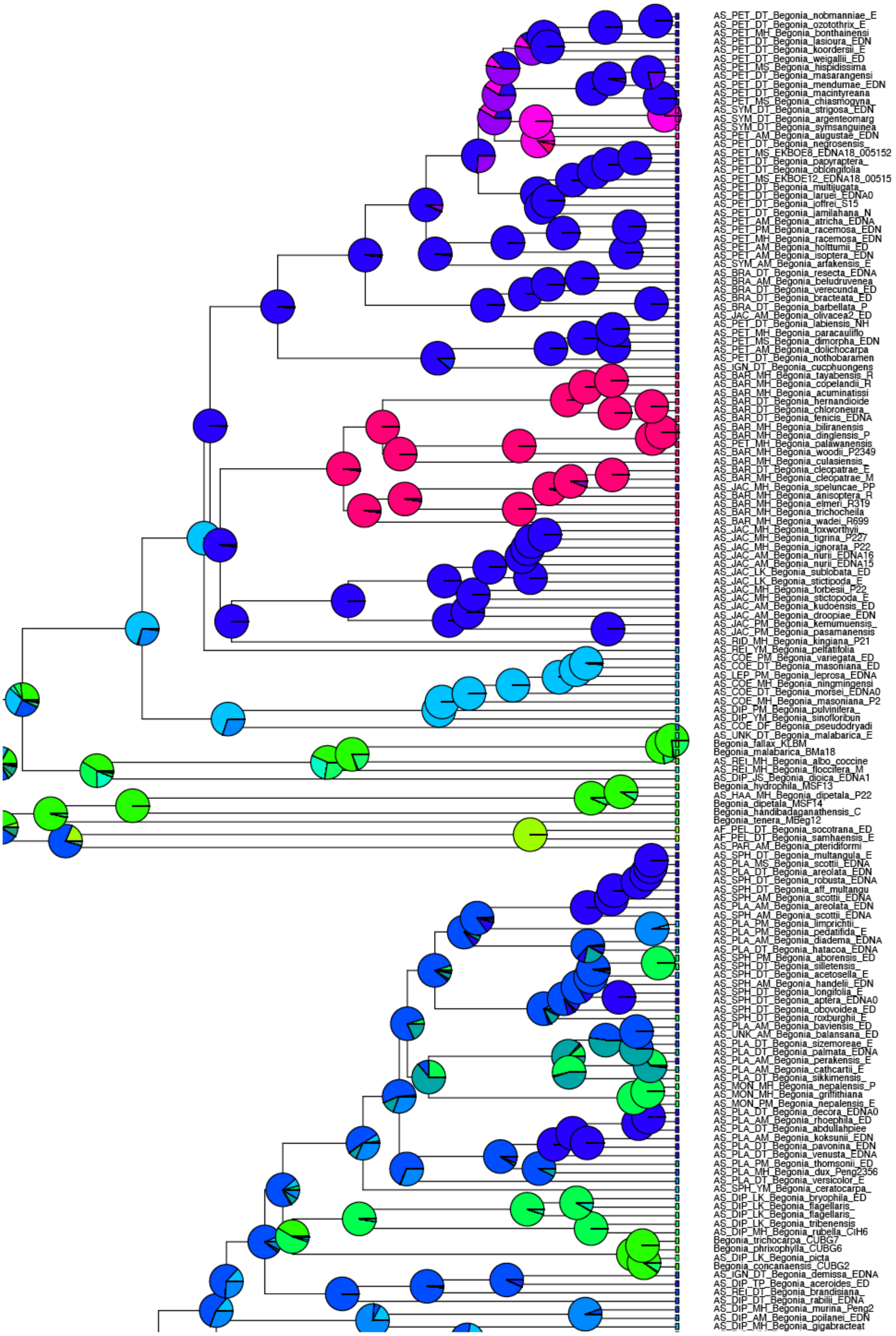
A.5.2 *Begoniaceae*

DEC+J Reconstruction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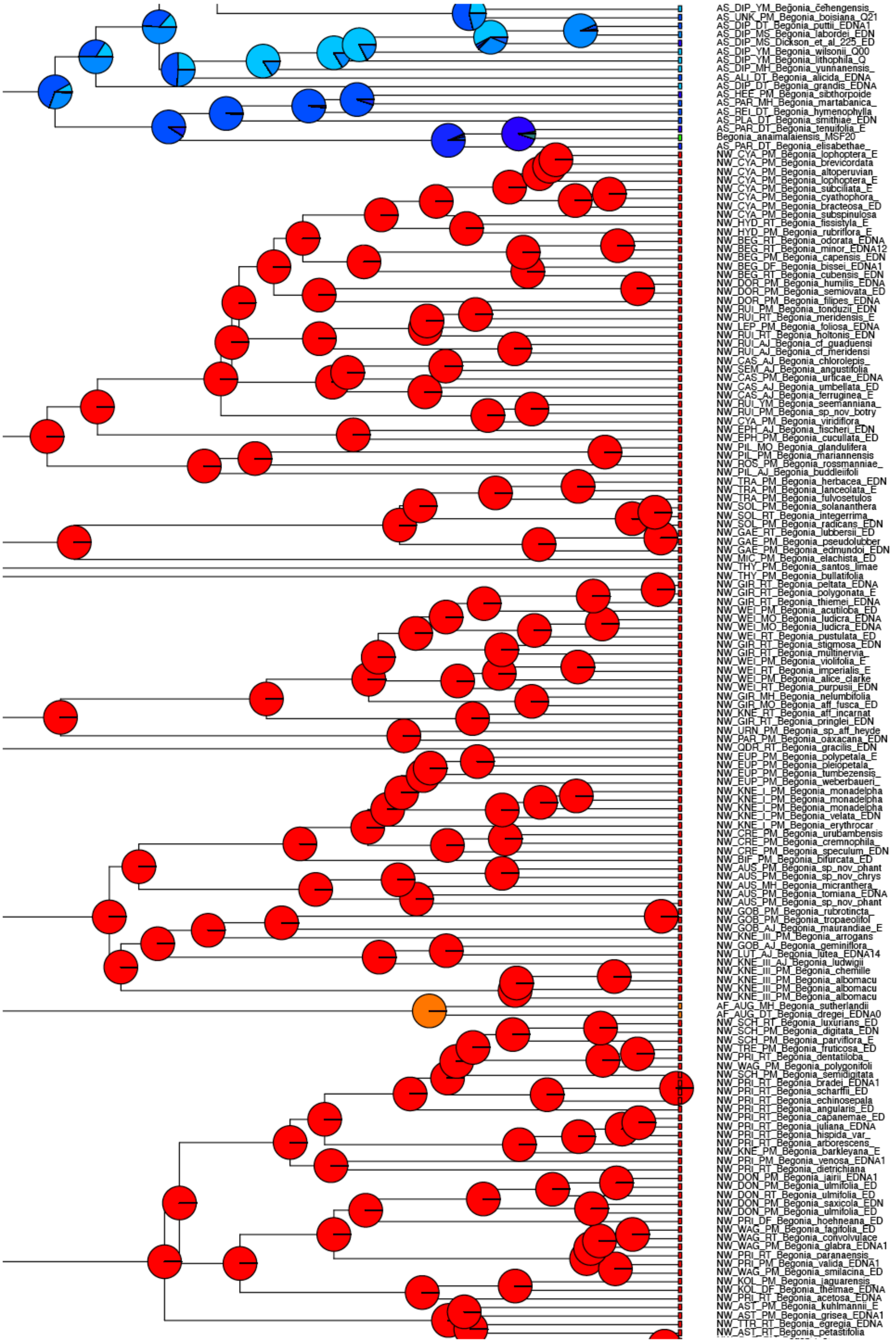
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NW_EUP_PM_Begonia_pleiopetala_
NW_EUP_PM_Begonia_tumbezensis_
NW_EUP_PM_Begonia_weberbaueri_
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NW_KNE_I_PM_Begonia_monadelpha
NW_KNE_I_PM_Begonia_monadelpha
NW_KNE_I_PM_Begonia_velata_EDN
NW_KNE_I_PM_Begonia_erythrocar
NW_CRE_PM_Begonia_urubambensis
NW_CRE_PM_Begonia_cremnophila_
NW_CRE_PM_Begonia_speculum_EDN
NW_BIF_PM_Begonia_bifurcata_ED
NW_AUS_PM_Begonia_sp_nov_phant
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NW_AUS_MH_Begonia_micranthera_
NW_AUS_PM_Begonia_tomiana_EDNA
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NW_GOB_PM_Begonia_rubrotincta_
NW_GOB_PM_Begonia_tropaeolifol
NW_GOB_AJ_Begonia_maurandiae_E
NW_KNE_III_PM_Begonia_arrogans
NW_GOB_AJ_Begonia_geminiflora_
NW_LUT_AJ_Begonia_lutea_EDNA14
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AF_AUG_DT_Begonia_dregei_EDNA0
NW_SCH_RT_Begonia_luxurians_ED
NW_SCH_PM_Begonia_digitata_EDN
NW_SCH_PM_Begonia_parviflora_E
NW_TRE_PM_Begonia_fruticosa_ED
NW_PRI_RT_Begonia_dentatiloba_
NW_WAG_PM_Begonia_polygonifoli
NW_SCH_PM_Begonia_semidigitata
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NW_PRI_RT_Begonia_echinosepala
NW_PRI_RT_Begonia_angularis_ED
NW_PRI_RT_Begonia_capanemae_ED
NW_PRI_RT_Begonia_juliana_EDNA
NW_PRI_RT_Begonia_hispida_var_
NW_PRI_RT_Begonia_arborescens_
NW_KNE_PM_Begonia_barkleyana_E
NW_PRI_PM_Begonia_venosa_EDNA1
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NW_DON_PM_Begonia_jairii_EDNA1
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NW_DON_RT_Begonia_ulmifolia_ED
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NW_DON_PM_Begonia_ulmifolia_ED
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NW_KOL_DF_Begonia_thelmae_EDNA
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NW_AST_PM_Begonia_kuhlmannii_E
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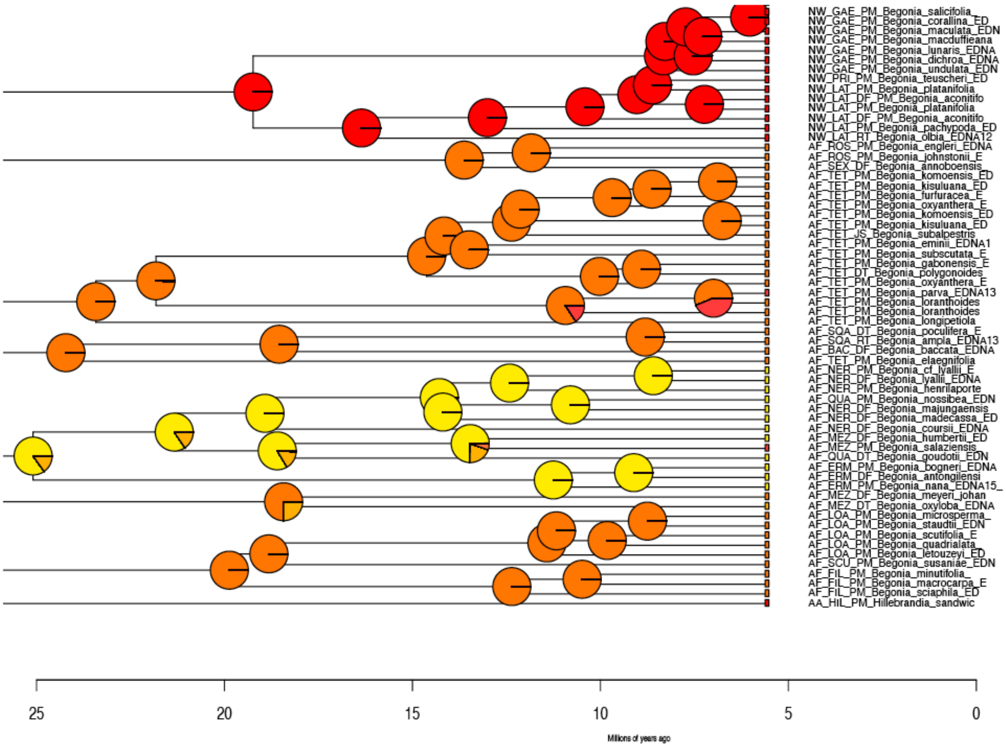

Figure A.2: DEC+J ancestral area reconstruction for the family *Begoniaceae.*

Log Likelihood Values

Model	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-436.8	2	0.0025	0.0013	0	877.5	3.1e-21
DEC+J	-388.5	3	0.0010	1.0e-12	0.0049	783.1	1.00
DIVALIKE	-402.5	3	0.0011	1.0e-12	0.0056	811	8.8e-07
DIVALIKE+J	-402.5	3	0.0011	1.0e-12	0.0055	811	8.8e-07
BAYAREALIKE	-412.1	3	0.0009	0.0012	0.0056	830.3	5.6e-11
BAYAREALIKE+J	-410.6	3	0.0008	1.0e-12	0.0064	827.1	2.7e-10

Table A.3: Log likelihood values for six biogeographic models run using BioGeoBEARS.

Scored Geography

```
372 13 (A B C D E F G H I J K L M)
AA_HIL_PM_Hillebrandia_sandwicensis_EDNA13_0034233 1000000000000
AF_AUG_DT_Begonia_dregei_EDNA09_02164 0100000000000
AF_AUG_MH_Begonia_sutherlandii_MH80 0100000000000
AF_BAC_DF_Begonia_baccata_EDNA14_0035689 0100000000000
AF_ERM_DF_Begonia_antongilensis_EDNA14_0035458 0010000000000
AF_ERM_PM_Begonia_bogneri_EDNA13_0033469 0010000000000
AF_ERM_PM_Begonia_nana_EDNA15_0039180 0010000000000
AF_FIL_PM_Begonia_macrocarpa_EDNA15_0039233 0100000000000
AF_FIL_PM_Begonia_minutifolia_EDNA15_0039688 0100000000000
AF_FIL_PM_Begonia_sciaphila_EDNA15_0039163 0100000000000
AF_LOA_PM_Begonia_letouzeyi_EDNA15_0039682 0100000000000
AF_LOA_PM_Begonia_microsperma_EDNA13_0033503 0100000000000
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AF_LOA_PM_Begonia_scutifolia_EDNA13_0033504 0100000000000
AF_LOA_PM_Begonia_staudtii_EDNA15_0039727 0100000000000
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AF_MEZ_DF_Begonia_meyeri_johannis_EDNA14_0035692 0100000000000
AF_MEZ_DT_Begonia_oxyloba_EDNA08_02841 0110000000000
AF_MEZ_PM_Begonia_salaziensis_EDNA15_0039164 0100000000001
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AF_NER_DF_Begonia_lyallii_EDNA14_0035459 0010000000000
AF_NER_DF_Begonia_madecassa_EDNA14_0035693 0010000000000
AF_NER_DF_Begonia_majungaensis_EDNA14_0035460 0010000000000
AF_NER_PM_Begonia_cf_lyallii_EDNA15_0039167 0010000000000
AF_NER_PM_Begonia_henrilaportei_EDNA15_0039172 0010000000000
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AF_PEL_DT_Begonia_socotrana_EDNA08_00210_ 0001000000000
AF_QUA_DT_Begonia_goudotii_EDNA09_02167 0010000000000
AF_QUA_PM_Begonia_nossibea_EDNA13_0033507 0010000000000
AF_ROS_PM_Begonia_engleri_EDNA13_0000001 0100000000000
AF_ROS_PM_Begonia_johnstonii_EDNA13_0000002 0100000000000
AF_SCU_PM_Begonia_susaniae_EDNA15_0039730 0100000000000
AF_SEX_DF_Begonia_annoboensis_EDNA14_0035690 0100000000000
AF_SQA_DT_Begonia_poculifera_EDNA09_02175 0100000000000
AF_SQA_RT_Begonia_ampla_EDNA13_0030222 0100000000000
AF_TET_DT_Begonia_polygonoides_EDNA09_02176 0100000000000
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NW_CYA_PM_Begonia_subciliata_EDNA16_0044357	1000000000000
NW_CYA_PM_Begonia_subspinulosa_EDNA15_0038868	1000000000000
NW_CYA_PM_Begonia_viridiflora_EDNA16_0044360	1000000000000
NW_DON_PM_Begonia_jairii_EDNA15_0039231	1000000000000
NW_DON_PM_Begonia_saxicola_EDNA15_0039719	1000000000000
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NW_DOR_PM_Begonia_filipes_EDNA15_0039174	1000000000000
NW_DOR_PM_Begonia_humilis_EDNA15_0039723	1000000000000
NW_DOR_PM_Begonia_semiovata_EDNA16_0044351	1000000000000
NW_EPH_AJ_Begonia_fischeri_EDNA14_0037193	1000000000000
NW_EPH_PM_Begonia_cucullata_EDNA15_0039658	1000000000000
NW_EUP_PM_Begonia_pleiopetala_EDNA16_0044380	1000000000000
NW_EUP_PM_Begonia_polypetala_EDNA16_0044328	1000000000000
NW_EUP_PM_Begonia_tumbezensis_EDNA14_0036874	1000000000000
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NW_GAE_PM_Begonia_edmundoi_EDNA13_0033068	1000000000000
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NW_GAE_PM_Begonia_macduffieana_EDNA13_	1000000000000
NW_GAE_PM_Begonia_maculata_EDNA13_0033069	1000000000000
NW_GAE_PM_Begonia_pseudolubbersii_EDNA13_0033073	1000000000000

NW_GAE_PM_Begonia_salicifolia_EDNA15_0039717	1000000000000
NW_GAE_PM_Begonia_undulata_EDNA13_0033513	1000000000000
NW_GAE_RT_Begonia_lubbersii_EDNA12_0025406	1000000000000
NW_GIR_MH_Begonia_nelumbifolia_P20879	1000000000000
NW_GIR_MO_Begonia_aff_fusca_EDNA15_0038388	1000000000000
NW_GIR_RT_Begonia_multinervia_EDNA12_0025412_	1000000000000
NW_GIR_RT_Begonia_peltata_EDNA12_0025405_	1000000000000
NW_GIR_RT_Begonia_polygonata_EDNA13_0030230	1000000000000
NW_GIR_RT_Begonia_pringlei_EDNA12_0025419	1000000000000
NW_GIR_RT_Begonia_stigmosa_EDNA12_0025423	1000000000000
NW_GIR_RT_Begonia_thiemei_EDNA13_0030234	1000000000000
NW_GOB_AJ_Begonia_geminiflora_EDNA14_0037177	1000000000000
NW_GOB_AJ_Begonia_maurandiae_EDNA14_0037191	1000000000000
NW_GOB_PM_Begonia_rubrotincta_EDNA16_0044331	1000000000000
NW_GOB_PM_Begonia_tropaeolifolia_EDNA16_0044341	1000000000000
NW_HYD_PM_Begonia_rubriflora_EDNA15_0039713	1000000000000
NW_HYD_RT_Begonia_fissistyla_EDNA12_0025392_	1000000000000
NW_KNE_I_PM_Begonia_erythrocarpa_EDNA15_0038870	1000000000000
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NW_KNE_I_PM_Begonia_velata_EDNA16_0044323	1000000000000
NW_KNE_III_AJ_Begonia_ludwigii_EDNA14_0036778	1000000000000
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NW_KNE_RT_Begonia_aff_incarnata_EDNA13_0030226	1000000000000
NW_KOL_DF_Begonia_thelmae_EDNA14_0035457	1000000000000
NW_KOL_PM_Begonia_jaguarensis_EDNA15_0039675	1000000000000
NW_LAT_DF_PM_Begonia_aconitifolia_EDNA13_0033499	1000000000000
NW_LAT_DF_PM_Begonia_aconitifolia_EDNA14_0036895	1000000000000
NW_LAT_PM_Begonia_pachypoda_EDNA13_0033079	1000000000000
NW_LAT_PM_Begonia_platanifolia_EDNA15_0038263	1000000000000
NW_LAT_PM_Begonia_platanifolia_EDNA15_0039242	1000000000000
NW_LAT_RT_Begonia_olbia_EDNA12_0025415_	1000000000000
NW_LEP_PM_Begonia_foliosa_EDNA13_0033092	1000000000000
NW_LUT_AJ_Begonia_lutea_EDNA14_0037171	1000000000000
NW_MIC_PM_Begonia_elachista_EDNA16_0045213	1000000000000
NW_PAR_PM_Begonia_oaxacana_EDNA14_0036900	1000000000000
NW_PIL_AJ_Begonia_buddleiifolia_EDNA14_0037195	1000000000000
NW_PIL_MO_Begonia_glandulifera_EDNA15_0038389	1000000000000
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NW_PRI_RT_Begonia_bradei_EDNA12_0025378	1000000000000
NW_PRI_RT_Begonia_capanemae_EDNA12_0025380	1000000000000
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NW_SCH_RT_Begonia_luxurians_EDNA12_0025407	1000000000000
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NW_SOL_PM_Begonia_radicans_EDNA13_0033070	1000000000000
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NW_SOL_RT_Begonia_integerrima_EDNA12_0025402	1000000000000
NW_THY_PM_Begonia_bullatifolia_EDNA15_0039680	1000000000000
NW_THY_PM_Begonia_santos_limae_EDNA13_0033491	1000000000000
NW_TRA_PM_Begonia_fulvosetulosa_EDNA15_0039664	1000000000000
NW_TRA_PM_Begonia_herbacea_EDNA13_0033099	1000000000000
NW_TRA_PM_Begonia_lanceolata_EDNA15_0039679	1000000000000
NW_TRE_PM_Begonia_fruticosa_EDNA15_0039173	1000000000000
NW_TTR_RT_Begonia_egregia_EDNA12_0025391_	1000000000000
NW_URN_PM_Begonia_sp_aff_heydei_EDNA13_0033489	1000000000000
NW_WAG_PM_Begonia_fagifolia_EDNA13_0033096	1000000000000
NW_WAG_PM_Begonia_glabra_EDNA13_0033482	1000000000000
NW_WAG_PM_Begonia_polygonifolia_EDNA15_0039705	1000000000000
NW_WAG_PM_Begonia_smilacina_EDNA15_0039724	1000000000000
NW_WAG_RT_Begonia_convolvulacea_EDNA12_0025384	1000000000000
NW_WEI_MO_Begonia_ludicra_EDNA15_0038391	1000000000000
NW_WEI_MO_Begonia_ludicra_EDNA15_0038392	1000000000000
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NW_WEI_PM_Begonia_alice_clarkea_EDNA13_0033094	1000000000000
NW_WEI_PM_Begonia_violifolia_EDNA15_0039738	1000000000000
NW_WEI_RT_Begonia_imperialis_EDNA12_0025400_	1000000000000
NW_WEI_RT_Begonia_purpusii_EDNA12_0025420	1000000000000
NW_WEI_RT_Begonia_pustulata_EDNA13_0030231	1000000000000

A.5.3 *Chloranthaceae*

DEC+J Reconstruction

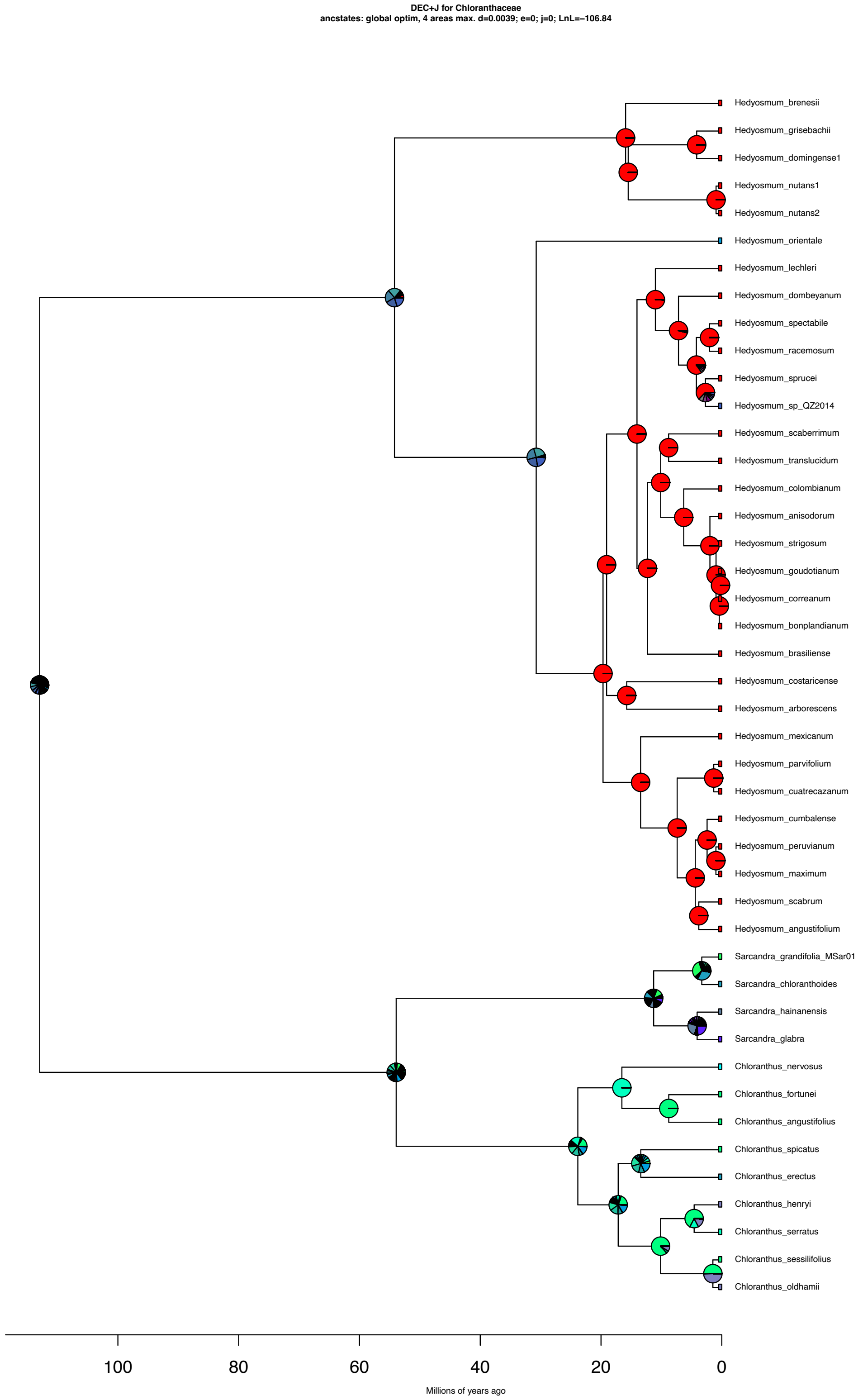


Figure A.3: DEC+J ancestral area reconstruction for the family *Chloranthaceae*.

Log Likelihood Values

Model	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-106.8	2	0.0039	1.0e-12	0	217.7	0.73
DEC+J	-106.8	3	0.0039	1.0e-12	1.0e-05	219.7	0.27
DIVALIKE	-111.8	3	0.0042	1.0e-12	1.0e-05	229.6	0.0019
DIVALIKE+J	-111.8	3	0.0042	1.6e-09	1.0e-05	229.6	0.0019

Table A.4: Log likelihood values for six biogeographic models run using BioGeoBEARS.

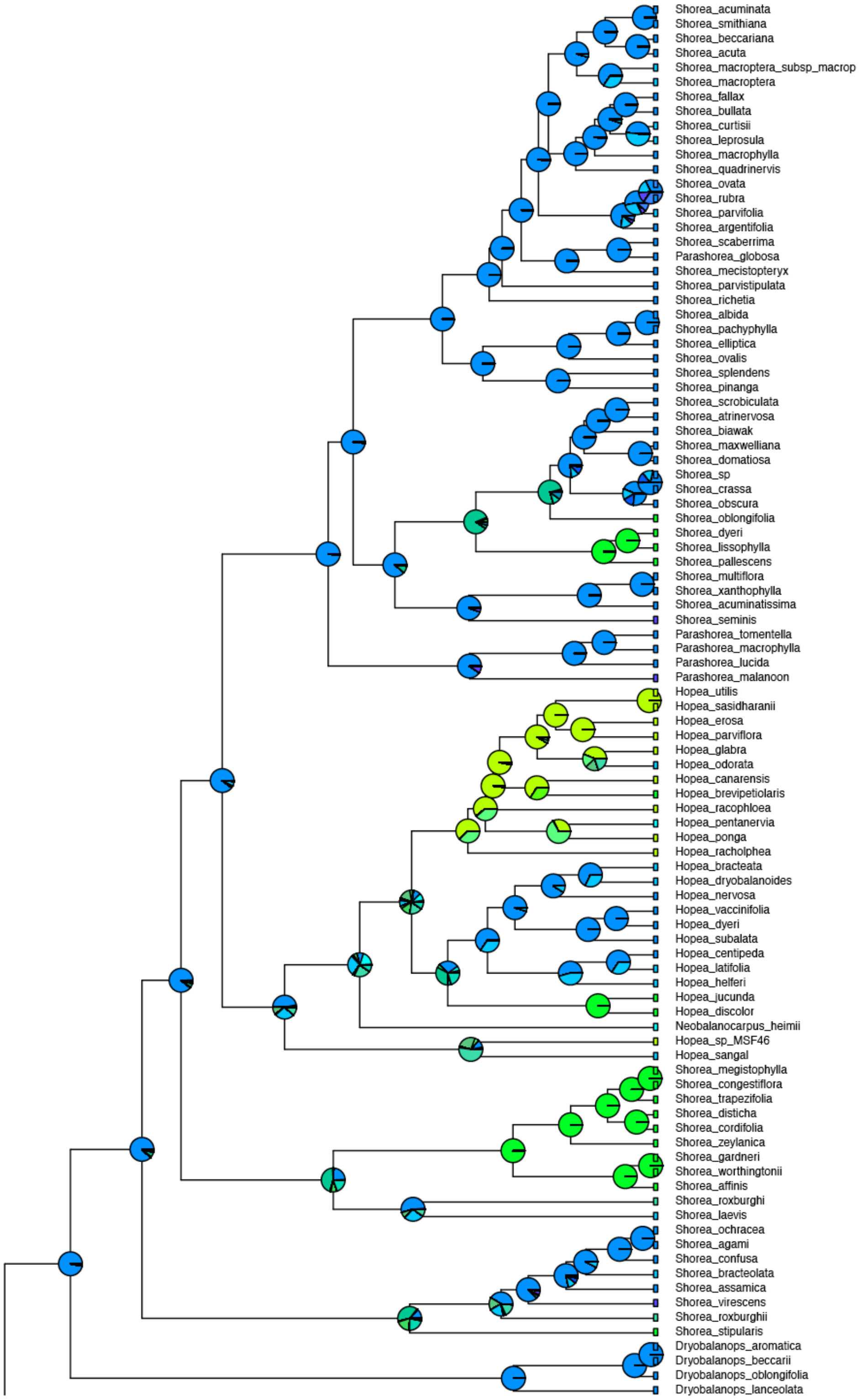
Scored Geography

```
44 12  (A    B    C    D    E    F    G    H    I    J    K    L)
Chloranthus_angustifolius 000001000000
Chloranthus_erectus 000100111000
Chloranthus_fortunei 000001000000
Chloranthus_henryi 000001000010
Chloranthus_nervosus 000000100000
Chloranthus_oldhamii 000001000010
Chloranthus_serratus 000001100000
Chloranthus_sessilifolius 000001000000
Chloranthus_spicatus 000001000000
Hedyosmum_angustifolium 100000000000
Hedyosmum_anisodorum 100000000000
Hedyosmum_arborescens 100000000000
Hedyosmum_bonplandianum 100000000000
Hedyosmum_brasiliense 100000000000
Hedyosmum_brenesii 100000000000
Hedyosmum_colombianum 100000000000
Hedyosmum_correanum 100000000000
Hedyosmum_costaricense 100000000000
Hedyosmum_cuatrecazanum 100000000000
Hedyosmum_cumbalense 100000000000
Hedyosmum_dombeyanum 100000000000
Hedyosmum_domingense1 100000000000
Hedyosmum_goudotianum 100000000000
Hedyosmum_grisebachii 100000000000
Hedyosmum_lechleri 100000000000
Hedyosmum_maximum 100000000000
Hedyosmum_mexicanum 100000000000
Hedyosmum_nutans1 100000000000
Hedyosmum_nutans2 100000000000
Hedyosmum_orientale 000001111000
```

Hedyosmum_parvifolium 100000000000
Hedyosmum_peruvianum 100000000000
Hedyosmum_racemosum 100000000000
Hedyosmum_scaberrimum 100000000000
Hedyosmum_scabrum 100000000000
Hedyosmum_sp_QZ2014 100000111000
Hedyosmum_spectabile 100000000000
Hedyosmum_sprucei 100000000000
Hedyosmum_strigosum 100000000000
Hedyosmum_translucidum 100000000000
Sarcandra_chloranthoides 000100111000
Sarcandra_glabra 000000011110
Sarcandra_hainanensis 000011000110
Sarcandra_grandifolia_MSar01 000111100000

A.5.4 *Dipterocarpaceae*

DEC+J Reconstruction


Shorea_acuminata
Shorea_smithiana
Shorea_beccariana
Shorea_acuta
Shorea_macroptera_subsp_macrop
Shorea_macroptera
Shorea_fallax
Shorea_bullata
Shorea_curtisii
Shorea_leprosula
Shorea_macrophylla
Shorea_quadrinervis
Shorea_ovata
Shorea_rubra
Shorea_parvifolia
Shorea_argentifolia
Shorea_scaberrima
Parashorea_globosa
Shorea_mecistopteryx
Shorea_parvistipulata
Shorea_richetia
Shorea_albida
Shorea_pachyphylla
Shorea_elliptica
Shorea_ovalis
Shorea_splendens
Shorea_pinanga
Shorea_scrobiculata
Shorea_atrinervosa
Shorea_biawak
Shorea_maxwelliana
Shorea_domatiosa
Shorea_sp
Shorea_crassa
Shorea_obscura
Shorea_oblongifolia
Shorea_dyeri
Shorea_lissophylla
Shorea_pallescens
Shorea_multiflora
Shorea_xanthophylla
Shorea_acuminatissima
Shorea_seminis
Parashorea_tomentella
Parashorea_macrophylla
Parashorea_lucida
Parashorea_malanoon
Hopea_utilis
Hopea_sasidharanii
Hopea_erosa
Hopea_parviflora
Hopea_glabra
Hopea_odorata
Hopea_canarensis
Hopea_brevipetiolaris
Hopea_racophloea
Hopea_pentanervia
Hopea_ponga
Hopea_racholphea
Hopea_bracteata
Hopea_dryobalanoides
Hopea_nervosa
Hopea_vaccinifolia
Hopea_dyeri
Hopea_subalata
Hopea_centipeda
Hopea_latifolia
Hopea_helferi
Hopea_jucunda
Hopea_discolor
Neobalanocarpus_heimii
Hopea_sp_MSF46
Hopea_sangal
Shorea_megistophylla
Shorea_congestiflora
Shorea_trapezifolia
Shorea_disticha
Shorea_cordifolia
Shorea_zeylanica
Shorea_gardneri
Shorea_worthingtonii
Shorea_affinis
Shorea_roxburghi
Shorea_laevis
Shorea_ochracea
Shorea_agami
Shorea_confusa
Shorea_bracteolata
Shorea_assamica
Shorea_virescens
Shorea_roxburghii
Shorea_stipularis
Dryobalanops_aromatica
Dryobalanops_beccarii
Dryobalanops_oblongifolia
Dryobalanops_lanceolata

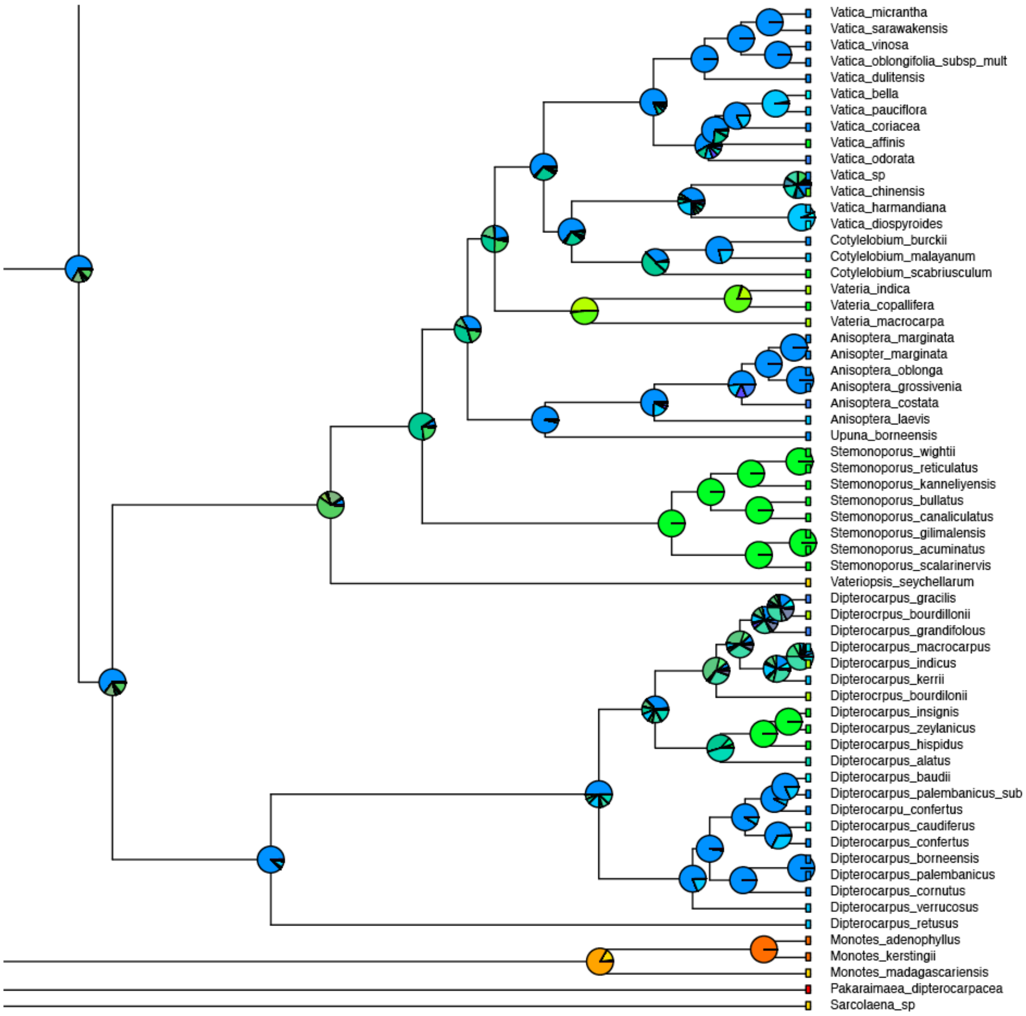


Figure A.4: DEC+J ancestral area reconstruction for the family *Dipterocarpaceae*.

Model	LnL	numparams	d	e	j
DEC	-395.08898532952	2	0.00121884720220535	0.000835076205355535	0
DEC+J	-390.052025167874	3	0.00103283231922687	1e-12	0.00342509756888097
DIVALIKE	-399.483569554207	3	0.0011626559004792	1.00000042970774e-12	0.00263091383860167
DIVALIKE+J	-399.48356143916	3	0.0011625524737548	2.33531180091844e-10	0.00264227095973346
BAYAREALIKE	-372.389821621515	3	0.000461754589035011	0.00590606292391973	0.00669712183229436
BAYAREALIKE+J	-372.517996266652	3	0.000481925398008236	0.00613504837476309	0.00583434274109458

Table A.5: Log likelihood values for six biogeographic models run using BioGeoBEARS.

Scored Geography

```
158 14 (A     B     C     D     E     F     G     H     I     J     K     L
        M     N)
Pakaraimaea_dipterocarpacea          10000000000000
Sarcolaena_sp                   00100000000000
Monotes_madagascariensis             00100000000000
Monotes_adenophyllus               01000000000000
Monotes_kerstingii              01000000000000
Dipterocarpus_retusus             00000001100000
Dipterocrpus_bourdilonii           00010000000000
Dipterocarpus_alatus             00000101100000
Dipterocarpus_hispidus            00000100000000
Dipterocarpus_insignis            00000100000000
Dipterocarpus_zeylanicus           00000100000000
Dipterocarpus_gracilis           00000001100100
Dipterocarpus_grandifolous          00000001100100
Dipterocarpus_kerrii            00000001100000
Dipterocarpus_indicus             00010000000000
Dipterocarpus_confertus            00000000100000
Dipterocrpus_bourdillonii          00010000000000
```

Dipterocarpus_macrocarpus	00000011100000
Dipterocarpus_baudii	00000001000000
Dipterocarpus_caudiferus	00000001000000
Dipterocarpus_palembanicus_subsp_borneensis	00000000100000
Dipterocarpus_verrucosus	00000001100000
Dipterocarpu_confertus	00000000100000
Dipterocarpus_cornutus	00000000100000
Dipterocarpus_palembanicus	00000000100000
Dipterocarpus_borneensis	00000000100000
Vateriopsis_seychellarum	00100000000000
Stemonoporus_bullatus	00000100000000
Stemonoporus_canaliculatus	00000100000000
Stemonoporus_wightii	00000100000000
Stemonoporus_reticulatus	00000100000000
Stemonoporus_kanneliyensis	00000100000000
Stemonoporus_scalarinervis	00000100000000
Stemonoporus_gilimalensis	00000100000000
Stemonoporus_acuminatus	00000100000000
Vateria_macrocarpa	00010000000000
Vateria_indica	00010000000000
Vateria_copallifera	00000100000000
Upuna_borneensis	00000000100000
Anisoptera_laevis	00000001100000
Anisoptera_marginata	00000000100000
Anisoptera_costata	00000001100100
Anisopter_marginata	00000000100000
Anisoptera_oblonga	00000000100000
Anisoptera_grossivenia	00000000100000
Cotylelobium_scabriusculum	00000100000000
Cotylelobium_malayanum	00000001100000
Cotylelobium_burckii	00000000100000
Vatica_diospyroides	00000001000000
Vatica_harmandiana	00000001100000
Vatica_sp	00000001110000
Vatica_chinensis	00010100000000
Vatica_dulitensis	00000000100000
Vatica_sarawakensis	00000000100000
Vatica_micrantha	00000000100000
Vatica_pauciflora	00000001100000
Vatica_bella	00000001000000
Vatica_vinosa	00000000100000
Vatica_oblongifolia_subsp_multinervosa	00000000100000
Vatica_odorata	00000001100100
Vatica_coriacea	00000000100000
Vatica_affinis	00000100000000
Dryobalanops_lanceolata	00000000100000
Dryobalanops_oblongifolia	00000000100000
Dryobalanops_beccarii	00000000100000

Dryobalanops_aromatica	00000000100000
Shorea_stipularis	00000100000000
Shorea_roxburghii	00010001100000
Shorea_virescens	00000000100100
Shorea_ochracea	00000000100000
Shorea_bracteolata	00000001100000
Shorea_assamica	00000001110000
Shorea_confusa	00000000100000
Shorea_agami	00000000100000
Hopea_sp_MSF46	00010000000000
Hopea_sangal	00000001100000
Neobalanocarpus_heimii	00000001000000
Hopea_racophloea	00010000000000
Hopea_canarensis	00010000000000
Hopea_brevipetiolaris	00000100000000
Hopea_ponga	00010000000000
Hopea_pentanervia	00000001000000
Hopea_racholphea	00010000000000
Hopea_parviflora	00010000000000
Hopea_erosa	00010000000000
Hopea_odorata	00000001100000
Hopea_glabra	00010000000000
Hopea_utilis	00010000000000
Hopea_sasidharanii	00010000000000
Hopea_discolor	00000100000000
Hopea_jucunda	00000100000000
Hopea_helferi	00000001100000
Hopea_latifolia	00000001100000
Hopea_centipeda	00000000100000
Hopea_nervosa	00000000100000
Hopea_dryobalanoides	00000001100000
Hopea_bracteata	00000001100000
Hopea_subalata	00000000100000
Hopea_dyeri	00000000100000
Hopea_vaccinifolia	00000000100000
Shorea_laevis	00000001100000
Shorea_roxburghi	00010001100000
Shorea_affinis	00000100000000
Shorea_worthingtonii	00000100000000
Shorea_gardneri	00000100000000
Shorea_zeylanica	00000100000000
Shorea_trapezifolia	00000100000000
Shorea_disticha	00000100000000
Shorea_cordifolia	00000100000000
Shorea_megistophylla	00000100000000
Shorea_congestiflora	00000100000000
Parashorea_malanoon	00000000100100
Parashorea_lucida	00000000100000

Parashorea_tomentella	00000000100000
Parashorea_macrophylla	00000000100000
Shorea_acuminatissima	00000000100000
Shorea_xanthophylla	00000000100000
Shorea_multiflora	00000000100000
Shorea_pallescens	00000100000000
Shorea_lissophylla	00000100000000
Shorea_dyeri	00000100000000
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Shorea_sp	00000001110000
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Shorea_maxwelliana	00000000100000
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Shorea_ovalis	00000000100000
Shorea_pachyphylla	00000000100000
Shorea_albida	00000000100000
Shorea_elliptica	00000000100000
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Shorea_mecistopteryx	00000000100000
Shorea_scaberrima	00000000100000
Parashorea_globosa	00000000100000
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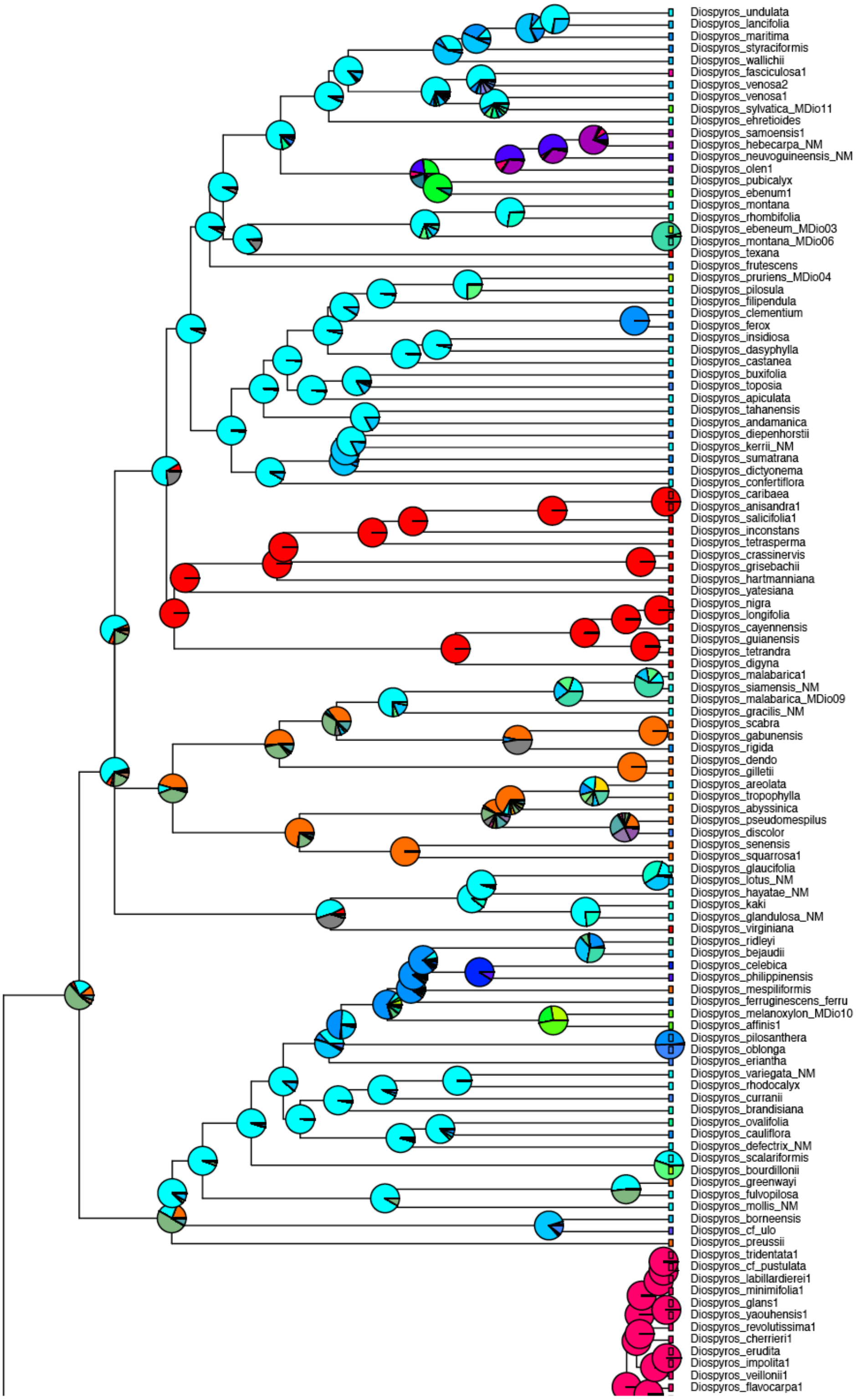
Shorea_fallax	00000000100000
Shorea_curtisii	00000001100000
Shorea_leprosula	00000001100000
Shorea_macrophylla	00000000100000
Shorea_bullata	00000000100000
Shorea_macroptera_subsp_macropterifolia	00000001100000
Shorea_macroptera	00000001100000
Shorea_acuminata	00000000100000
Shorea_acuta	00000000100000
Shorea_beccariana	00000000100000
Shorea_smithiana	00000000100000
Shorea_parvifolia	00000001100000
Shorea_argentifolia	00000000100000
Shorea_rubra	00000000100000
Shorea_ovata	00000001100100

A.5.5 *Ebenaceae*

DEC+J Reconstruction



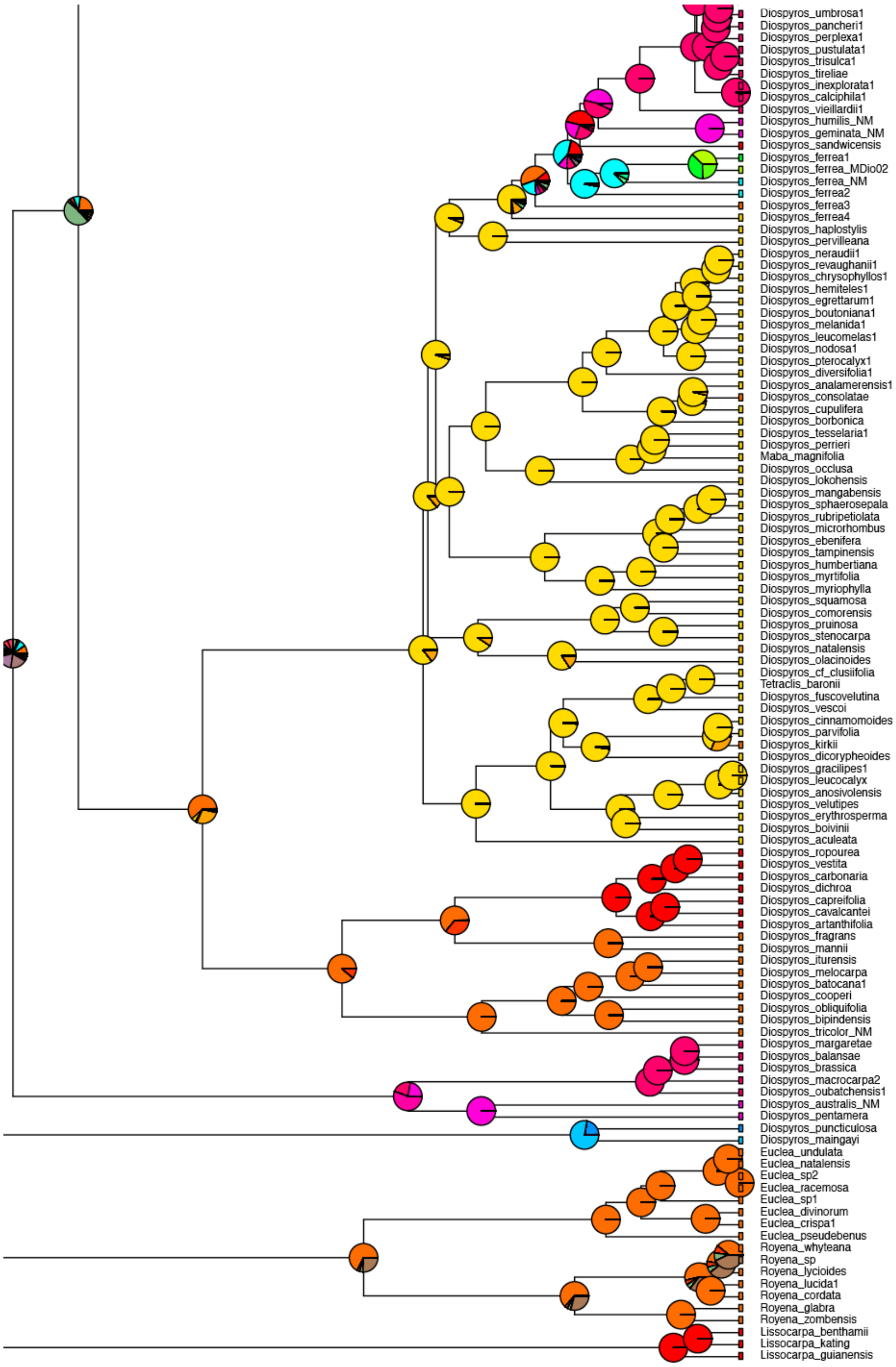


Figure A.5: DEC+J ancestral area reconstruction for the family *Ebenaceae*.

Model	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-536.8	2	0.0015	0.0015	0	1078	3.2e-18
DEC+J	-518.3	3	0.0011	1.0e-12	0.0058	1043	1.2e-10
DIVALIKE	-534.2	3	0.0014	1.0e-12	0.0044	1074	1.6e-17
DIVALIKE+J	-534.2	3	0.0014	2.7e-10	0.0044	1074	1.6e-17
BAYAREALIKE	-496	3	0.0005	0.0062	0.0075	998	0.62
BAYAREALIKE+J	-496.5	3	0.0005	0.0066	0.0062	999	0.38

Log Likelihood Values

Table A.4: Log likelihood values for six biogeographic models run using BioGeoBEARS.

Scored Geography

```
228 14 (A	B	C	D	E	F	G	H	I	J	K	L	M	N)

Lissocarpa_guianensis		10000000000000
Lissocarpa_kating		10000000000000
Lissocarpa_benthamii		10000000000000
Royena_zombensis		01000000000000
Royena_glabra		01000000000000
Royena_cordata		01000000000000
Royena_lucida1		01000000000000
Royena_lycioides		01000000000000
Royena_sp		11000001000000
Royena_whyteana		01000000000000
Euclea_pseudebenus		01000000000000
Euclea_crispa1		01000000000000
Euclea_divinorum		01000000000000
Euclea_sp1		01000000000000
Euclea_racemosa		01000000000000
Euclea_sp2		01000000000000
Euclea_natalensis		01000000000000
Euclea_undulata		01000000000000
Diospyros_maingayi		00000001100000
Diospyros_puncticulosa		00000000100000
```

Diospyros_pentamera	0000000000010
Diospyros_australis_NM	0000000000010
Diospyros_oubatchensis1	0000000000001
Diospyros_macrocarpa2	0000000000001
Diospyros_brassica	0000000000001
Diospyros_balansae	0000000000001
Diospyros_margaretae	0000000000001
Diospyros_tricolor_NM	0100000000000
Diospyros_bipindensis	0100000000000
Diospyros_obliquifolia	0100000000000
Diospyros_cooperi	0100000000000
Diospyros_batocana1	0100000000000
Diospyros_melocarpa	0100000000000
Diospyros_iturensis	0100000000000
Diospyros_mannii	0100000000000
Diospyros_fragrans	0100000000000
Diospyros_artanthifolia	1000000000000
Diospyros_cavalcantei	1000000000000
Diospyros_capreifolia	1000000000000
Diospyros_dichroa	1000000000000
Diospyros_carbonaria	1000000000000
Diospyros_vestita	1000000000000
Diospyros_ropourea	1000000000000
Diospyros_aculeata	0010000000000
Diospyros_boivinii	0010000000000
Diospyros_erythrosperma	0010000000000
Diospyros_velutipes	0010000000000
Diospyros_anosivolensis	0010000000000
Diospyros_leucocalyx	0010000000000
Diospyros_gracilipes1	0010000000000
Diospyros_dicorypheoides	0010000000000
Diospyros_kirkii	0100000000000
Diospyros_parvifolia	0010000000000
Diospyros_cinnamomoides	0010000000000
Diospyros_vescoi	0010000000000
Diospyros_fuscovelutina	0010000000000
Tetraclis_baronii	0010000000000
Diospyros_cf_clusiifolia	0010000000000
Diospyros_olacinoides	0010000000000
Diospyros_natalensis	0110000000000
Diospyros_stenocarpa	0010000000000
Diospyros_pruinosa	0010000000000
Diospyros_comorensis	0010000000000
Diospyros_squamosa	0010000000000
Diospyros_myriophylla	0010000000000
Diospyros_myrtifolia	0010000000000
Diospyros_humbertiana	0010000000000
Diospyros_tampinensis	0010000000000

Diospyros_ebenifera	00100000000000
Diospyros_microrhombus	00100000000000
Diospyros_rubripetiolata	00100000000000
Diospyros_sphaerosepala	00100000000000
Diospyros_mangabensis	00100000000000
Diospyros_lokohensis	00100000000000
Diospyros_occlusa	00100000000000
Maba_magnifolia	00100000000000
Diospyros_perrieri	00100000000000
Diospyros_tesselaria1	00100000000000
Diospyros_borbonica	00100000000000
Diospyros_cupulifera	00100000000000
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Diospyros_analamerensis1	00100000000000
Diospyros_diversifolia1	00100000000000
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Diospyros_nodosa1	00100000000000
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Diospyros_boutoniana1	00100000000000
Diospyros_egrettarum1	00100000000000
Diospyros_hemiteles1	00100000000000
Diospyros_chrysophyllos1	00100000000000
Diospyros_revaughanii1	00100000000000
Diospyros_neraudii1	00100000000000
Diospyros_pervilleana	00100000000000
Diospyros_haplostylis	00100000000000
Diospyros_ferrea4	00100000000000
Diospyros_ferrea3	01000000000000
Diospyros_ferrea2	00000001000000
Diospyros_ferrea_NM	00000001000000
Diospyros_ferrea_MDio02	00010000000000
Diospyros_ferrea1	00000100000000
Diospyros_sandwicensis	10000000000000
Diospyros_geminata_NM	00000000000010
Diospyros_humilis_NM	00000000000010
Diospyros_vieillardii1	00000000000001
Diospyros_calciphila1	00000000000001
Diospyros_inexplorata1	00000000000001
Diospyros_tireliae	00000000000001
Diospyros_trisulca1	00000000000001
Diospyros_pustulata1	00000000000001
Diospyros_perplexa1	00000000000001
Diospyros_pancheri1	00000000000001
Diospyros_umbrosa1	00000000000001
Diospyros_flavocarpa1	00000000000001
Diospyros_veillonii1	00000000000001
Diospyros_impolita1	00000000000001

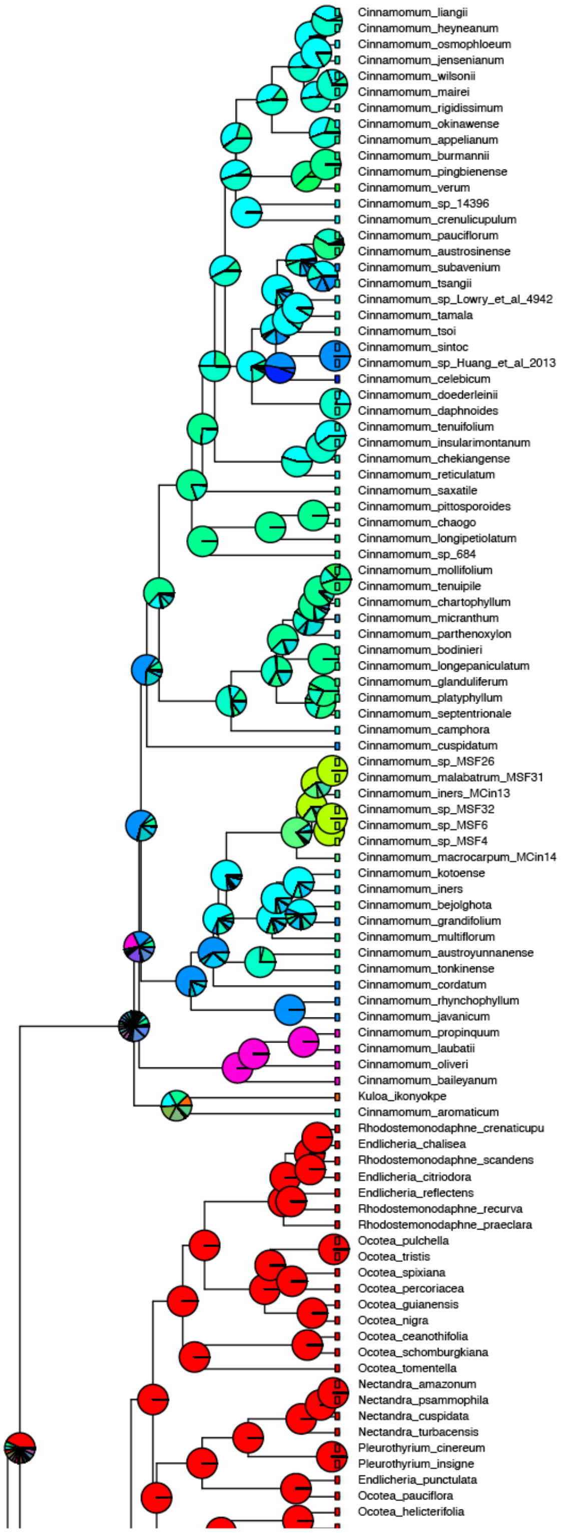
```
Diospyros_erudita                 00000000000001
Diospyros_cherrieri1               00000000000001
Diospyros_revolutissima1              00000000000001
Diospyros_yaouhensis1               00000000000001
Diospyros_glans1                  00000000000001
Diospyros_minimifolia1              00000000000001
Diospyros_labillardierei1            00000000000001
Diospyros_cf_pustulata              00000000000001
Diospyros_tridentata1               00000000000001
Diospyros_preussii                01000000000000
Diospyros_cf_ulo                  00000000100100
Diospyros_borneensis                00000001100000
Diospyros_mollis_NM                 00000001000000
Diospyros_fulvopilosa               00000001000000
Diospyros_greenwayi                 01000000000000
Diospyros_bourdillonii              00010000000000
Diospyros_scalariformis             00000001000000
Diospyros_defectrix_NM                00000001000000
Diospyros_cauliflora               00000001110000
Diospyros_ovalifolia               00000101000000
Diospyros_brandisiana               00000011000000
Diospyros_curranii                00000001100100
Diospyros_rhodocalyx                00000001000000
Diospyros_variegata_NM                00000001000000
Diospyros_eriantha                00000001100100
Diospyros_oblonga                  00000001100100
Diospyros_pilosanthera              00000001110000
Diospyros_affinis1                00010100000000
Diospyros_melanoxylon_MDio10          00010100000000
Diospyros_ferruginescens_ferruginescens   00000000100000
Diospyros_mespiliformis              01000000000000
Diospyros_philippinensis             00000000010100
Diospyros_celebica                 00000000010000
Diospyros_bejaudii                00000001100000
Diospyros_ridleyi                 00010001100000
Diospyros_virginiana               10000000000000
Diospyros_glandulosa_NM              00000001000000
Diospyros_kaki                   00000011000000
Diospyros_hayatae_NM                00000001000000
Diospyros_lotus_NM                 00000001100000
Diospyros_glaucifolia              00000011000000
Diospyros_squarrosa1                01000000000000
Diospyros_senensis                 01000000000000
Diospyros_discolor                 00000001100100
Diospyros_pseudomespilus              01000000000000
Diospyros_abyssinica               01000000000000
Diospyros_tropophylla               00100000000000
Diospyros_areolata                 00000001100000
```

Diospyros_gilletii	01000000000000
Diospyros_dendo	01000000000000
Diospyros_rigida	00000000100000
Diospyros_gabunensis	01000000000000
Diospyros_scabra	01000000000000
Diospyros_gracilis_NM	00000001000000
Diospyros_malabarica_MDio09	00010001100000
Diospyros_siamensis_NM	00000001000000
Diospyros_malabarica1	00010001100000
Diospyros_digyna	10000000000000
Diospyros_tetrandra	10000000000000
Diospyros_guianensis	10000000000000
Diospyros_cayennensis	10000000000000
Diospyros_longifolia	10000000000000
Diospyros_nigra	10000000000000
Diospyros_yatesiana	10000000000000
Diospyros_hartmanniana	10000000000000
Diospyros_grisebachii	10000000000000
Diospyros_crassinervis	10000000000000
Diospyros_tetrasperma	10000000000000
Diospyros_inconstans	10000000000000
Diospyros_salicifolia1	10000000000000
Diospyros_anisandra1	10000000000000
Diospyros_caribaea	10000000000000
Diospyros_confertiflora	00000001000000
Diospyros_dictyonema	00000000100000
Diospyros_sumatrana	00000001110000
Diospyros_kerrii_NM	00000001000000
Diospyros_diepenhorstii	00000001100100
Diospyros_andamanica	00000001100000
Diospyros_tahanensis	00000001100000
Diospyros_apiculata	00000001000000
Diospyros_toposia	00000001100100
Diospyros_buxifolia	00000001110000
Diospyros_castanea	00000001000000
Diospyros_dasyphylla	00000001000000
Diospyros_insidiosa	00000001100000
Diospyros_ferox	00000000100000
Diospyros_clementium	00000000100000
Diospyros_filipendula	00000001000000
Diospyros_pilosula	00000001000000
Diospyros_pruriens_MDio04	00010000000000
Diospyros_frutescens	00000001110000
Diospyros_texana	10000000000000
Diospyros_montana_MDio06	00010001100000
Diospyros_ebeneum_MDio03	00010000000000
Diospyros_rhombifolia	00000010000000
Diospyros_montana	00000001000000

Diospyros_ebenum1	00000100000000
Diospyros_pubicalyx	00000100010000
Diospyros_olen1	00000000001001
Diospyros_neuvoguineensis_NM	00000000001000
Diospyros_hebecarpa_NM	00000000010011
Diospyros_samoensis1	00000000001001
Diospyros_ehretioides	00000001000000
Diospyros_sylvatica_MDio11	00010100000000
Diospyros_venosa1	00000001100000
Diospyros_venosa2	00000001100000
Diospyros_fasciculosa1	00000000000011
Diospyros_wallichii	00000001100000
Diospyros_styraciformis	00000000100000
Diospyros_maritima	00000001110000
Diospyros_lancifolia	00000001100000
Diospyros_undulata	00000001000000

A.5.6 *Lauraceae*

DEC+J Reconstruction


Cinnamomum_liangii
Cinnamomum_heyneanum
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Cinnamomum_jensenianum
Cinnamomum_wilsonii
Cinnamomum_mairei
Cinnamomum_rigidissimum
Cinnamomum_okinawense
Cinnamomum_appelianum
Cinnamomum_burmannii
Cinnamomum_pingbienense
Cinnamomum_verum
Cinnamomum_sp_14396
Cinnamomum_crenulicupulum
Cinnamomum_pauciflorum
Cinnamomum_austrosinense
Cinnamomum_subavenium
Cinnamomum_tsangii
Cinnamomum_sp_Lowry_et_al_4942
Cinnamomum_tamala
Cinnamomum_tsoi
Cinnamomum_sintoc
Cinnamomum_sp_Huang_et_al_2013
Cinnamomum_celebicum
Cinnamomum_doederleinii
Cinnamomum_daphnoides
Cinnamomum_tenuifolium
Cinnamomum_insularimontanum
Cinnamomum_chekiangense
Cinnamomum_reticulatum
Cinnamomum_saxatile
Cinnamomum_pittosporoides
Cinnamomum_chaogo
Cinnamomum_longipetiolatum
Cinnamomum_sp_684
Cinnamomum_mollifolium
Cinnamomum_tenuipile
Cinnamomum_chartophyllum
Cinnamomum_micranthum
Cinnamomum_parthenoxylon
Cinnamomum_bodinieri
Cinnamomum_longepaniculatum
Cinnamomum_glanduliferum
Cinnamomum_platyphyllum
Cinnamomum_septentrionale
Cinnamomum_camphora
Cinnamomum_cuspidatum
Cinnamomum_sp_MSF26
Cinnamomum_malabatrum_MSF31
Cinnamomum_iners_MCin13
Cinnamomum_sp_MSF32
Cinnamomum_sp_MSF6
Cinnamomum_sp_MSF4
Cinnamomum_macrocarpum_MCin14
Cinnamomum_kotoense
Cinnamomum_iners
Cinnamomum_bejolghota
Cinnamomum_grandifolium
Cinnamomum_multiflorum
Cinnamomum_austroyunnanense
Cinnamomum_tonkinense
Cinnamomum_cordatum
Cinnamomum_rhynchophyllum
Cinnamomum_javanicum
Cinnamomum_propinquum
Cinnamomum_laubatii
Cinnamomum_oliveri
Cinnamomum_baileyanum
Kuloa_ikonyokpe
Cinnamomum_aromaticum
Rhodostemonodaphne_crenaticupu
Endlicheria_chalisea
Rhodostemonodaphne_scandens
Endlicheria_citriodora
Endlicheria_reflectens
Rhodostemonodaphne_recurva
Rhodostemonodaphne_praeclara
Ocotea_pulchella
Ocotea_tristis
Ocotea_spixiana
Ocotea_percoriacea
Ocotea_guianensis
Ocotea_nigra
Ocotea_ceanothifolia
Ocotea_schomburgkiana
Ocotea_tomentella
Nectandra_amazonum
Nectandra_psammophila
Nectandra_cuspidata
Nectandra_turbacensis
Pleurothyrium_cinereum
Pleurothyrium_insigne
Endlicheria_punctulata
Ocotea_pauciflora
Ocotea_helicterifolia

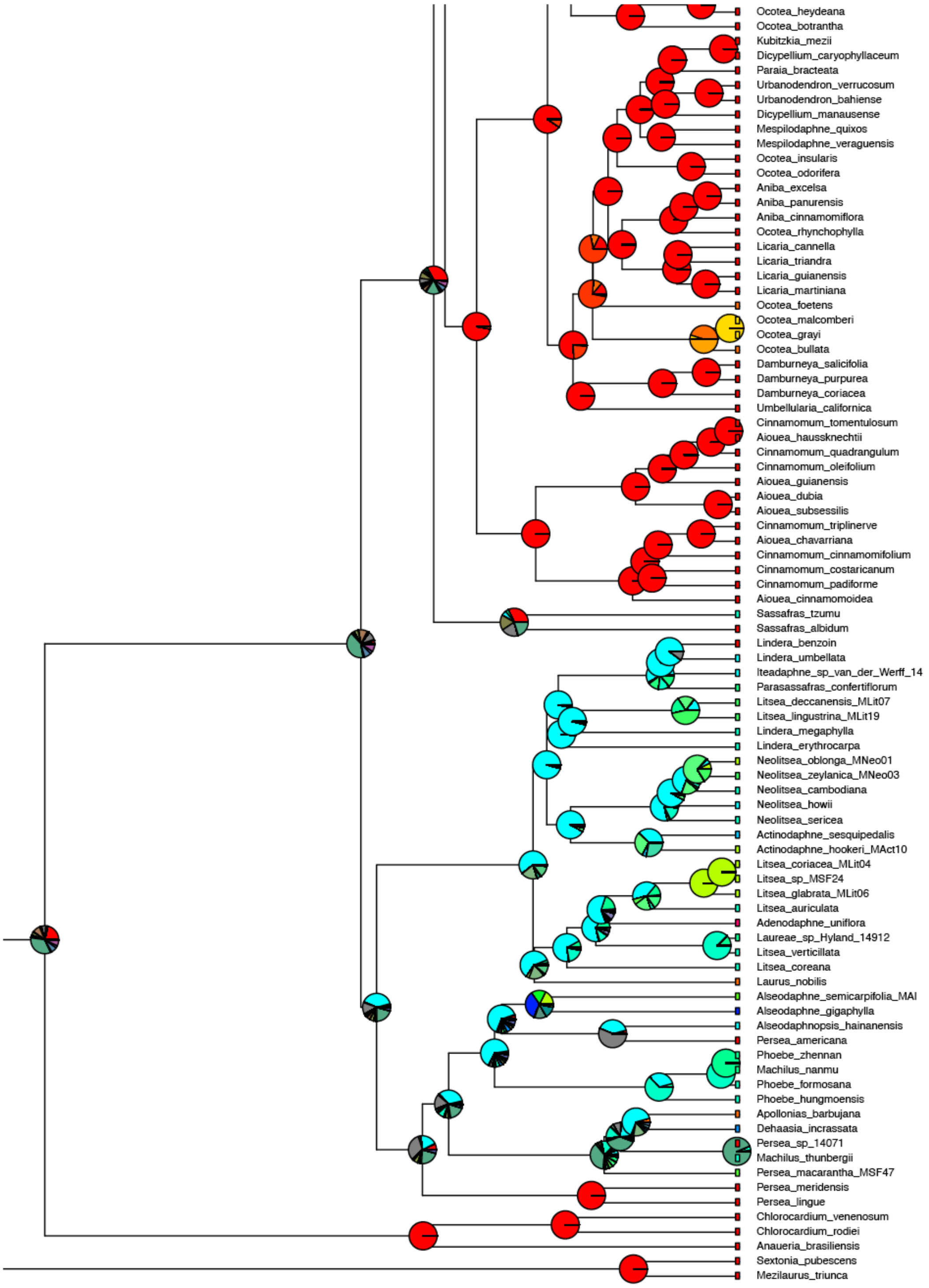

Figure A.6: DEC+J ancestral area reconstruction for the family *Lauraceae*.

Log Likelihood Values

Model	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-486.5	2	0.0032	0.0044	0	977.1	1.1e-24
DEC+J	-479.4	3	0.0025	1.0e-12	0.0049	964.9	4.8e-22
DIVALIKE	-502.4	3	0.0029	1.0e-12	0.0046	1011	5.3e-32
DIVALIKE+J	-502.4	3	0.0029	1.0e-12	0.0046	1011	5.3e-32
BAYAREALIKE	-431.1	3	0.0011	0.020	0.0053	868.1	0.50
BAYAREALIKE+J	-431.1	3	0.0011	0.020	0.0052	868.1	0.50

Table A.5: Log likelihood values for six biogeographic models run using BioGeoBEARS.

Scored Geography

182 14 (A B C D E F G H I J K L M N)

Mezilaurus_triunca	10000000000000
Sextonia_pubescens	10000000000000
Anaueria_brasiliensis	10000000000000
Chlorocardium_rodiei	10000000000000
Chlorocardium_venenosum	10000000000000
Persea_lingue	10000000000000
Persea_meridensis	10000000000000
Persea_macarantha_MSF47	00011010000000
Machilus_thunbergii	00000011000000
Persea_sp_14071	10000000000000
Dehaasia_incrassata	00000001110000
Apollonias_barbujana	01000000000000
Phoebe_hungmoensis	00000011000000
Phoebe_formosana	00000011000000
Machilus_nanmu	00000010000000
Phoebe_zhennan	00000010000000
Persea_americana	10000000000000
Alseodaphnopsis_hainanensis	00000001000000
Alseodaphne_gigaphylla	00000000010000
Alseodaphne_semicarpifolia_MAls12	00010100000000
Laurus_nobilis	01000000000000
Litsea_coreana	00000011000000
Litsea_verticillata	00000011000000
Laureae_sp_Hyland_14912	00000010000000
Adenodaphne_uniflora	00000000000001

```
Litsea_auriculata            00000011000000
Litsea_glabrata_MLit06          00010000000000
Litsea_sp_MSF24              00010000000000
Litsea_coriacea_MLit04          00010000000000
Actinodaphne_hookeri_MAct10     00010000000000
Actinodaphne_sesquipedalis      00000001100000
Neolitsea_sericea            00000011000000
Neolitsea_howii              00000001000000
Neolitsea_cambodiana           00000011000000
Neolitsea_zeylanica_MNeo03      00010101000000
Neolitsea_oblonga_MNeo01        00010000000000
Lindera_erythrocarpa           00000011000000
Lindera_megaphylla             00000011000000
Litsea_lingustrina_MLit19       00010101000000
Litsea_deccanensis_MLit07       00010101000000
Parasassafras_confertiflorum    00001011000000
Iteadaphne_sp_van_der_Werff_14360   00000001000000
Lindera_umbellata              00000001000000
Lindera_benzoin              10000000000000
Sassafras_albidum             10000000000000
Sassafras_tzumu              00000011000000
Aiouea_cinnamomoidea           10000000000000
Cinnamomum_padiforme           10000000000000
Cinnamomum_costaricanum         10000000000000
Cinnamomum_cinnamomifolium      10000000000000
Aiouea_chavarriana             10000000000000
Cinnamomum_triplinerve          10000000000000
Aiouea_subsessilis            10000000000000
Aiouea_dubia                10000000000000
Aiouea_guianensis             10000000000000
Cinnamomum_oleifolium          10000000000000
Cinnamomum_quadrangulum         10000000000000
Aiouea_haussknechtii           10000000000000
Cinnamomum_tomentulosum         10000000000000
Umbellularia_californica        10000000000000
Damburneya_coriacea            10000000000000
Damburneya_purpurea             10000000000000
Damburneya_salicifolia          10000000000000
Ocotea_bullata              01000000000000
Ocotea_grayi               00100000000000
Ocotea_malcomberi              00100000000000
Ocotea_foetens              01000000000000
Licaria_martiniana             10000000000000
Licaria_guianensis             10000000000000
Licaria_triandra             10000000000000
Licaria_cannella             10000000000000
Ocotea_rhynchophylla           10000000000000
Aniba_cinnamomiflora           10000000000000
```

Aniba_panurensis	10000000000000
Aniba_excelsa	10000000000000
Ocotea_odorifera	10000000000000
Ocotea_insularis	10000000000000
Mespilodaphne_veraguensis	10000000000000
Mespilodaphne_quixos	10000000000000
Dicypellium_manausense	10000000000000
Urbanodendron_bahiense	10000000000000
Urbanodendron_verrucosum	10000000000000
Paraia_bracteata	10000000000000
Dicypellium_caryophyllaceum	10000000000000
Kubitzkia_mezii	10000000000000
Ocotea_botrantha	10000000000000
Ocotea_heydeana	10000000000000
Ocotea_helicterifolia	10000000000000
Ocotea_pauciflora	10000000000000
Endlicheria_punctulata	10000000000000
Pleurothyrium_insigne	10000000000000
Pleurothyrium_cinereum	10000000000000
Nectandra_turbacensis	10000000000000
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Nectandra_amazonum	10000000000000
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Ocotea_ceanothifolia	10000000000000
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Ocotea_guianensis	10000000000000
Ocotea_percoriacea	10000000000000
Ocotea_spixiana	10000000000000
Ocotea_tristis	10000000000000
Ocotea_pulchella	10000000000000
Rhodostemonodaphne_praeclara	10000000000000
Rhodostemonodaphne_recurva	10000000000000
Endlicheria_reflectens	10000000000000
Endlicheria_citriodora	10000000000000
Rhodostemonodaphne_scandens	10000000000000
Endlicheria_chalisea	10000000000000
Rhodostemonodaphne_crenaticupula	10000000000000
Cinnamomum_aromaticum	00000011000000
Kuloa_ikonyokpe	01000000000000
Cinnamomum_baileyanum	00000000000010
Cinnamomum_oliveri	00000000000010
Cinnamomum_laubatii	00000000000010
Cinnamomum_propinquum	00000000000010
Cinnamomum_javanicum	00000000100000
Cinnamomum_rhynchophyllum	00000000100000
Cinnamomum_cordatum	00000000100000

```
Cinnamomum_tonkinense          00000011000000
Cinnamomum_austroyunnanense      00000010000000
Cinnamomum_multiflorum          00000101000000
Cinnamomum_grandifolium         00000000100000
Cinnamomum_bejolghota          00001011000000
Cinnamomum_iners             00000011100000
Cinnamomum_kotoense           00000001000000
Cinnamomum_macrocarpum_MCin14    00010001000000
Cinnamomum_sp_MSF4            00010000000000
Cinnamomum_sp_MSF6            00010000000000
Cinnamomum_sp_MSF32           00010000000000
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Cinnamomum_malabatrum_MSF31      00010000000000
Cinnamomum_sp_MSF26           00010000000000
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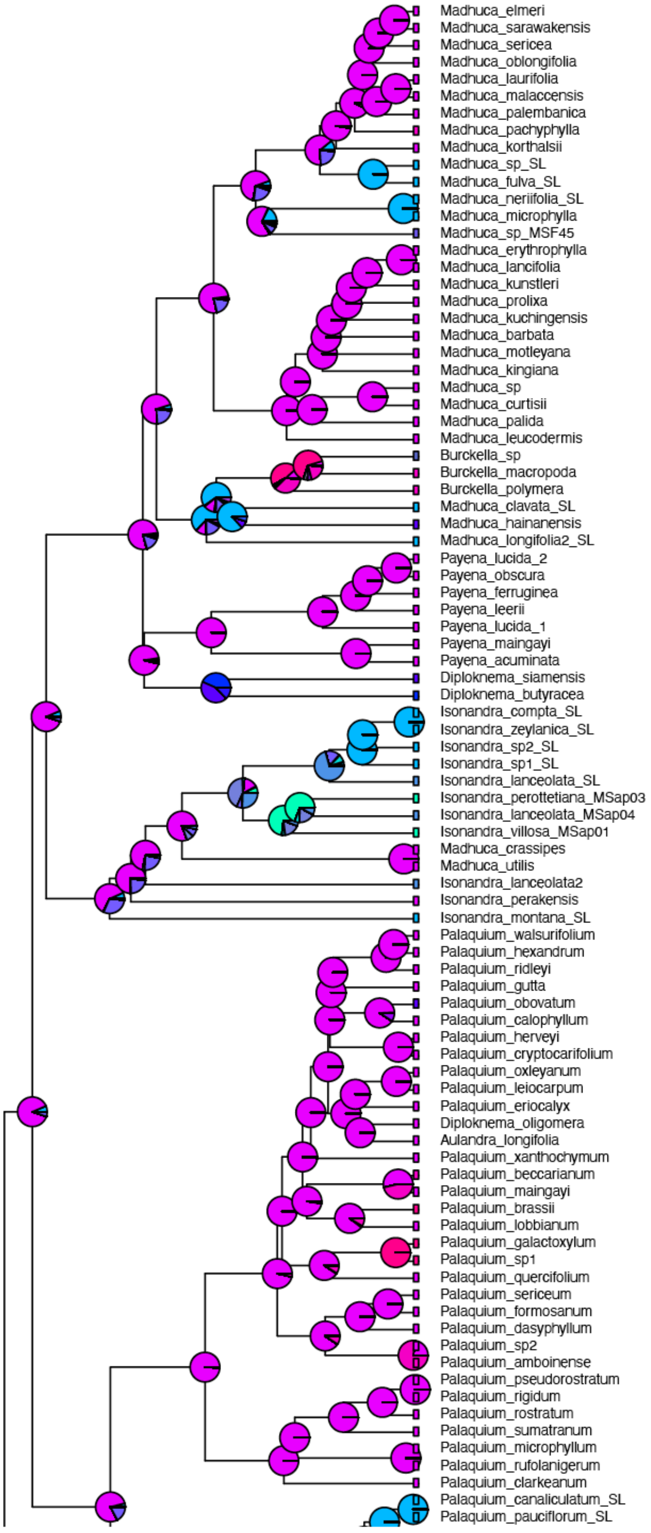
Cinnamomum_septentrionale       00000010000000
Cinnamomum_platyphyllum         00000010000000
Cinnamomum_glanduliferum        00001011000000
Cinnamomum_longepaniculatum      00000010000000
Cinnamomum_bodinieri          00000010000000
Cinnamomum_parthenoxylon        00000011100000
Cinnamomum_micranthum          00000011000100
Cinnamomum_chartophyllum        00000010000000
Cinnamomum_tenuipile          00001011000000
Cinnamomum_mollifolium         00000010000000
Cinnamomum_sp_684            00000010000000
Cinnamomum_longipetiolatum       00000010000000
Cinnamomum_chaogo            00000010000000
Cinnamomum_pittosporoides       00000010000000
Cinnamomum_saxatile           00000010000000
Cinnamomum_reticulatum         00000001000000
Cinnamomum_chekiangense         00000011000000
Cinnamomum_insularimontanum      00000001000000
Cinnamomum_tenuifolium         00000011000000
Cinnamomum_daphnoides          00000011000000
Cinnamomum_doederleinii         00000001000000
Cinnamomum_celebicum          00000000010000
Cinnamomum_sp_Huang_et_al_201310      00000000100000
Cinnamomum_sintoc            00000000100000
Cinnamomum_tsoi            00000011000000
Cinnamomum_tamala            00000011000000
Cinnamomum_sp_Lowry_et_al_4942   00000001000000
Cinnamomum_tsangii           00000011000000
Cinnamomum_subavenium          00000001110000
Cinnamomum_austrosinense        00000010000000
Cinnamomum_pauciflorum         00001011000000
Cinnamomum_crenulicupulum       00000001000000
```

Cinnamomum_sp_14396	00000001000000
Cinnamomum_verum	00000100000000
Cinnamomum_pingbienense	00000010000000
Cinnamomum_burmannii	00000010000000
Cinnamomum_appelianum	00000010000000
Cinnamomum_okinawense	00000001000000
Cinnamomum_rigidissimum	00000011000000
Cinnamomum_mairei	00000011000000
Cinnamomum_wilsonii	00000011000000
Cinnamomum_jensenianum	00000011000000
Cinnamomum_osmophloeum	00000001000000
Cinnamomum_heyneanum	00000011000000
Cinnamomum_liangii	00000011000000

A.5.7 *Sapotaceae*

DEC+J Reconstruction


Madhuca_elmeri
Madhuca_sarawakensis
Madhuca_sericea
Madhuca_oblongifolia
Madhuca_laurifolia
Madhuca_malaccensis
Madhuca_palembanica
Madhuca_pachyphylla
Madhuca_korthalsii
Madhuca_sp_SL
Madhuca_fulva_SL
Madhuca_neriifolia_SL
Madhuca_microphylla
Madhuca_sp_MSF45
Madhuca_erythrophylla
Madhuca_lancifolia
Madhuca_kunstleri
Madhuca_prolixa
Madhuca_kuchingensis
Madhuca_barbata
Madhuca_motleyana
Madhuca_kingiana
Madhuca_sp
Madhuca_curtisii
Madhuca_palida
Madhuca_leucodermis
Burckella_sp
Burckella_macropoda
Burckella_polymera
Madhuca_clavata_SL
Madhuca_hainanensis
Madhuca_longifolia2_SL
Payena_lucida_2
Payena_obscura
Payena_ferruginea
Payena_leerii
Payena_lucida_1
Payena_maingayi
Payena_acuminata
Diploknema_siamensis
Diploknema_butyracea
Isonandra_compta_SL
Isonandra_zeylanica_SL
Isonandra_sp2_SL
Isonandra_sp1_SL
Isonandra_lanceolata_SL
Isonandra_perottetiana_MSap03
Isonandra_lanceolata_MSap04
Isonandra_villosa_MSap01
Madhuca_crassipes
Madhuca_utilis
Isonandra_lanceolata2
Isonandra_perakensis
Isonandra_montana_SL
Palaquium_walsurifolium
Palaquium_hexandrum
Palaquium_ridleyi
Palaquium_gutta
Palaquium_obovatum
Palaquium_calophyllum
Palaquium_herveyi
Palaquium_cryptocarifolium
Palaquium_oxleyanum
Palaquium_leiocarpum
Palaquium_eriocalyx
Diploknema_oligomera
Aulandra_longifolia
Palaquium_xanthochymum
Palaquium_beccarianum
Palaquium_maingayi
Palaquium_brassii
Palaquium_lobbianum
Palaquium_galactoxylum
Palaquium_sp1
Palaquium_quercifolium
Palaquium_sericeum
Palaquium_formosanum
Palaquium_dasyphyllum
Palaquium_sp2
Palaquium_amboinense
Palaquium_pseudorostratum
Palaquium_rigidum
Palaquium_rostratum
Palaquium_sumatranum
Palaquium_microphyllum
Palaquium_rufolanigerum
Palaquium_clarkeanum
Palaquium_canaliculatum_SL
Palaquium_pauciflorum_SL

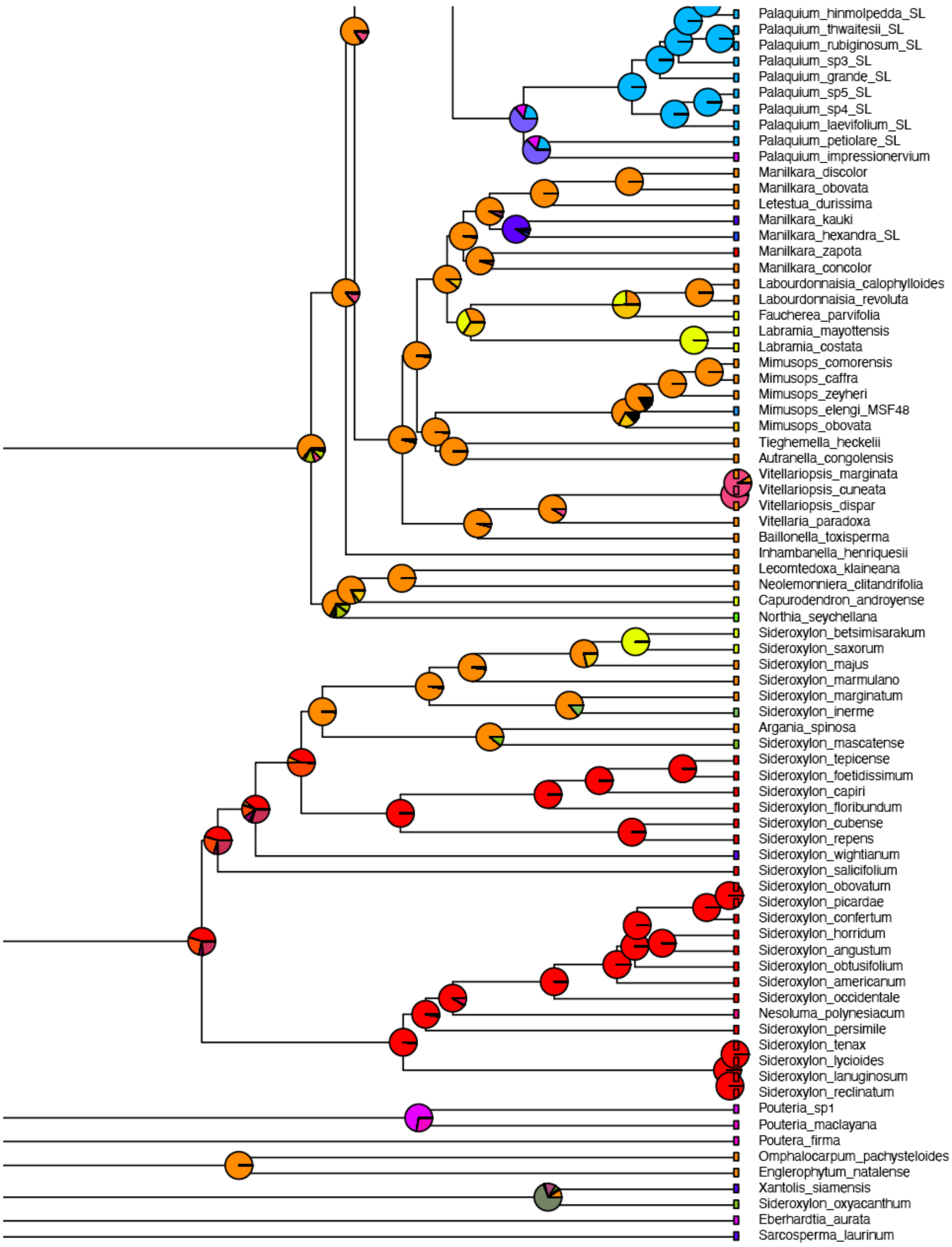


Figure A.7: DEC+J ancestral area reconstruction for the family *Sapotaceae*.

Log Likelihood Values

Model	LnL	numparams	d	e	j	AIC	AIC_wt
DEC	-313.8	2	0.0016	0.0025	0	631.6	8.2e-09
DEC+J	-294.2	3	0.0010	1.0e-12	0.0084	594.4	1.00
DIVALIKE	-302.6	3	0.0010	1.0e-12	0.0095	611.2	0.0002
DIVALIKE+J	-302.6	3	0.0010	1.0e-12	0.0091	611.1	0.0002
BAYAREALIKE	-312.7	3	0.0007	1.0e-12	0.014	631.3	9.4e-09
BAYAREALIKE+J	-312.3	3	0.0008	1.5e-10	0.013	630.7	1.3e-08

Table A.6: Log likelihood values for six biogeographic models run using BioGeoBEARS.

Scored Geography

```
167 11 (A	B	C	D	E	F	G	H	I	J	K)
Sarcosperma_laurinum	00000000100
Eberhardtia_aurata	00000000010
Xantolis_siamensis	00000000100
Sideroxylon_oxyacanthum	01001000000
Palaquium_laevifolium_SL	00000010000
Isonandra_lanceolata_SL	00000110010
Nesoluma_polynesiacum 00000000001
Sideroxylon_americanum	10000000000
Sideroxylon_horridum	10000000000
Sideroxylon_obovatum	10000000000
Sideroxylon_obtusifolium	10000000000
Sideroxylon_picardae	10000000000
Sideroxylon_occidentale	10000000000
Sideroxylon_angustum	10000000000
Sideroxylon_lanuginosum	10000000000
Sideroxylon_lycioides	10000000000
Sideroxylon_persimile	10000000000
Sideroxylon_reclinatum	10000000000
Sideroxylon_tenax	10000000000
Sideroxylon_confertum	10000000000
Argania_spinosa	01000000000
Sideroxylon_betsimisarakum	00100000000
Sideroxylon_capiri	10000000000
Sideroxylon_cubense	10000000000
Sideroxylon_floribundum	10000000000
Sideroxylon_foetidissimum	10000000000
```

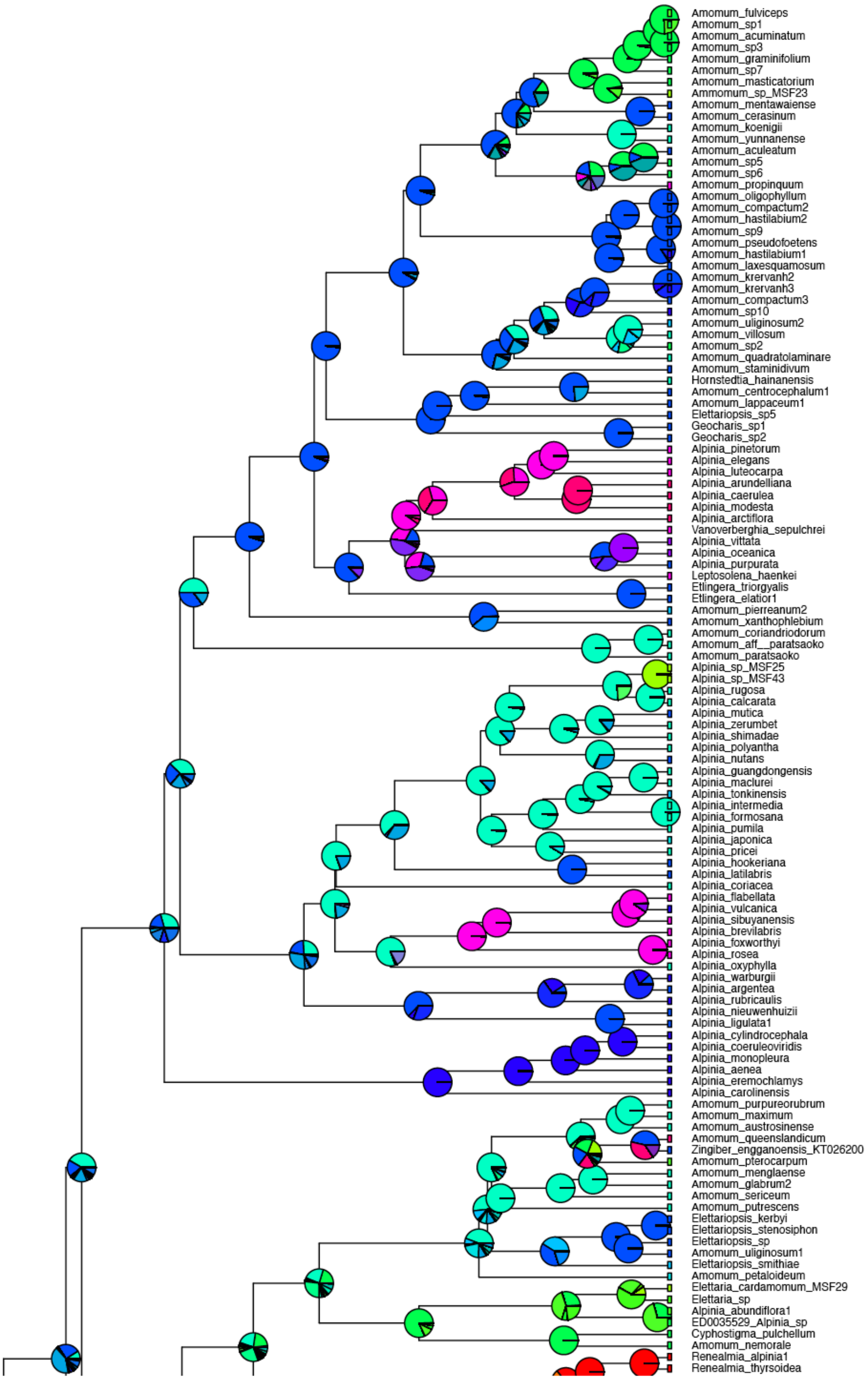
Sideroxylon_inerme	01000100000
Sideroxylon_majus	01000000000
Sideroxylon_marginatum	01000000000
Sideroxylon_marmulano	01000000000
Sideroxylon_mascatense	01001000000
Sideroxylon_repens	10000000000
Sideroxylon_salicifolium	10000000000
Sideroxylon_saxorum	00100000000
Sideroxylon_tepicense	10000000000
Sideroxylon_wightianum	00000000100
Omphalocarpum_pachysteloides	01000000000
Lecomtedoxa_klaineana	01000000000
Englerophytum_natalense	01000000000
Poutera_firma	00000000011
Pouteria_maclayana	00000000011
Pouteria_sp1	00000000010
Neolemonniera_clitandrifolia	01000000000
Northia_seychellana	00010000000
Capurodendron_androyense	00100000000
Madhuca_sp_SL	00000010000
Madhuca_fulva_SL	00000010000
Madhuca_neriifolia_SL	00000010000
Madhuca_longifolia2_SL	00000010000
Madhuca_crassipes	00000000010
Madhuca_utilis	00000000010
Aulandra_longifolia	00000000010
Palaquium_amboinense	00000000011
Palaquium_beccarianum	00000000011
Diploknema_oligomera	00000000010
Palaquium_brassii	00000000001
Palaquium_clarkeanum	00000000010
Palaquium_cryptocarifolium	00000000010
Palaquium_dasyphyllum	00000000010
Palaquium_eriocalyx	00000000010
Palaquium_formosanum	00000000010
Palaquium_galactoxylum	00000000001
Palaquium_gutta	00000000010
Palaquium_herveyi	00000000010
Palaquium_impressionervium	00000000010
Palaquium_leiocarpum	00000000010
Palaquium_lobbianum	00000000010
Palaquium_hexandrum	00000000010
Palaquium_maingayi	00000000010
Palaquium_microphyllum	00000000010
Palaquium_obovatum	00000000100
Palaquium_oxleyanum	00000000010
Palaquium_pseudorostratum	00000000010
Palaquium_quercifolium	00000000010

```
Palaquium_ridleyi	00000000010
Palaquium_rigidum	00000000010
Palaquium_rostratum	00000000010
Palaquium_rufolanigerum	00000000010
Palaquium_sericeum	00000000010
Palaquium_sp1	00000000001
Palaquium_sp2	00000000010
Palaquium_sumatranum	00000000010
Palaquium_walsurifolium	00000000010
Palaquium_calophyllum	00000000010
Palaquium_xanthochymum	00000000010
Palaquium_thwaitesii_SL	00000010000
Palaquium_canaliculatum_SL	00000010000
Palaquium_hinmolpedda_SL	00000010000
Palaquium_pauciflorum_SL	00000010000
Palaquium_rubiginosum_SL	00000010000
Isonandra_montana_SL	00000010000
Isonandra_sp1_SL	00000010000
Palaquium_sp3_SL	00000010000
Palaquium_grande_SL	00000010000
Palaquium_petiolare_SL	00000010000
Palaquium_sp5_SL	00000010000
Isonandra_sp2_SL	00000010000
Isonandra_compta_SL	00000010000
Isonandra_lanceolata2	00000110010
Isonandra_perakensis	00000000010
Isonandra_zeylanica_SL	00000010000
Autranella_congolensis	01000000000
Tieghemella_heckelii	01000000000
Vitellaria_paradoxa	01000000000
Vitellariopsis_cuneata	01000000010
Vitellariopsis_dispar	01000000000
Vitellariopsis_marginata	01000000000
Faucherea_parvifolia	00100000000
Inhambanella_henriquesii	01000000000
Baillonella_toxisperma	01000000000
Labourdonnaisia_calophylloides	01000000000
Labourdonnaisia_revoluta	01000000000
Labramia_costata	00100000000
Labramia_mayottensis	00100000000
Letestua_durissima	01000000000
Manilkara_hexandra_SL	00000011100
Manilkara_concolor	01000000000
Manilkara_discolor	01000000000
Manilkara_kauki	00000000100
Manilkara_obovata	01000000000
Manilkara_zapota	10000000000
Mimusops_caffra	01000000000
```

Mimusops_comorensis	01000000000
Mimusops_obovata	01100000000
Mimusops_zeyheri	01000000000
Burckella_macropoda	00000000011
Burckella_polymera	00000000011
Burckella_sp	00000101001
Diploknema_butyracea	00000001000
Diploknema_siamensis	00000000100
Madhuca_barbata	00000000010
Madhuca_curtisii	00000000010
Madhuca_elmeri	00000000010
Madhuca_erythrophylla	00000000010
Madhuca_hainanensis	00000000100
Madhuca_kingiana	00000000010
Madhuca_korthalsii	00000000010
Madhuca_kuchingensis	00000000010
Madhuca_kunstleri	00000000010
Madhuca_lancifolia	00000000010
Madhuca_laurifolia	00000000010
Madhuca_leucodermis	00000000010
Madhuca_malaccensis	00000000010
Madhuca_microphylla	00000010000
Madhuca_motleyana	00000000010
Madhuca_oblongifolia	00000000010
Madhuca_pachyphylla	00000000011
Madhuca_palembanica	00000000010
Madhuca_palida	00000000010
Madhuca_prolixa	00000000010
Madhuca_sarawakensis	00000000010
Madhuca_sericea	00000000010
Madhuca_sp	00000000010
Payena_acuminata	00000000010
Madhuca_clavata_SL	00000010000
Palaquium_sp4_SL	00000010000
Payena_lucida_1	00000000010
Payena_maingayi	00000000010
Payena_leerii	00000000010
Payena_ferruginea	00000000010
Payena_lucida_2	00000000010
Payena_obscura	00000000010
Mimusops_elengi_MSF48	00000110100
Isonandra_villosa_MSap01	00000100000
Isonandra_lanceolata_MSap04	00000110010
Isonandra_perottetiana_MSap03	00000100000
Madhuca_sp_MSF45	00000100110

A.4.8 *Zingiberaceae*

DEC+J Reconstruction



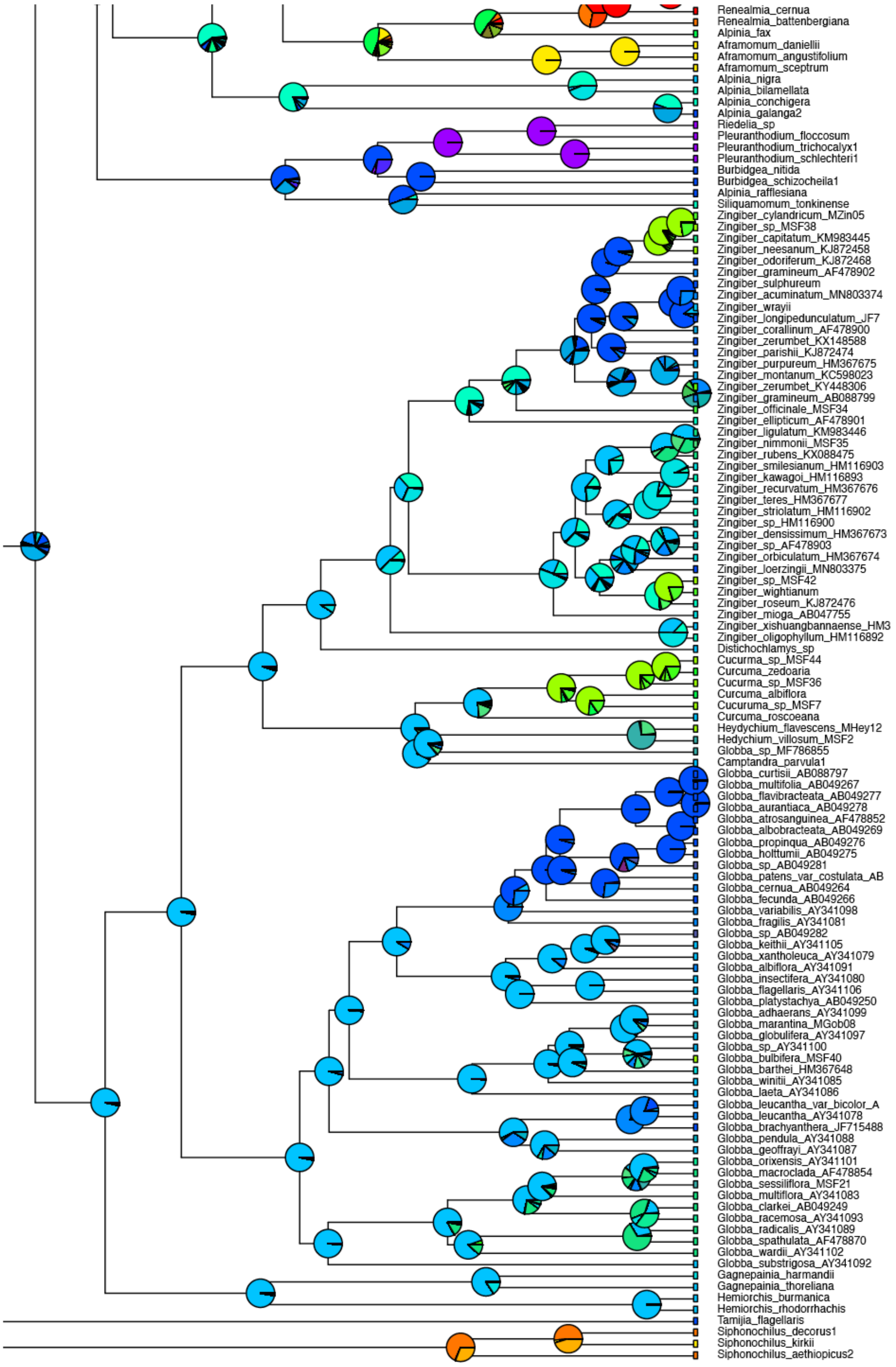


Figure A.8: DEC+J ancestral area reconstruction for the family *Zingiberaceae*.

Log Likelihood Values

Model	LnL	numparams	d	e	j	AIC	AIC_wt
1	-716.6	2	0.0038	0.0008	0	1437	2.2e-12
2	-688.7	3	0.0027	1.0e-12	0.012	1383	1.00
3	-704.8	3	0.0032	1.0e-12	0.0096	1416	1.1e-07
4	-704.8	3	0.0032	1.0e-12	0.0096	1416	1.1e-07

Table A.7: Log likelihood values for four biogeographic models run using BioGeoBEARS.

Scored Geography

238 13 (A B C D E F G H I J K L M)

Alpinia_abundiflora1	0001010000000
Amomum_fulviceps	0001010000000
Amomum_masticatorium	0000010000000
Amomum_pterocarpum	0001010000000
Curcuma_zedoaria	0000110000000
Elettaria_sp	0001110000000
Hedychium_villosum_MSF2	0001000110000
Zingiber_wightianum	0001010000000
Globba_marantina_MGob08	0001000110000
Zingiber_cylandricum_MZin05	0001010000000
Globba_spathulata_AF478870	0000100100000
Globba_multiflora_AY341083	0000100100000
Globba_racemosa_AY341093	0000101100000
Globba_orixensis_AY341101	0000101100000
Globba_clarkei_AB049249	0000100100000
Globba_platystachya_AB049250	0000000100000
Globba_sp_AB049281	1000000110000
Globba_sp_AB049282	1000000110000
Globba_macroclada_AF478854	0000100100000
Zingiber_sp_AF478903	0000100110000
Globba_radicalis_AY341089	0000100100000
Globba_globulifera_AY341097	0000000100000
Globba_sp_AY341100	0000001110000
Globba_wardii_AY341102	0000100100000
Zingiber_sp_HM116900	0000100110000
Globba_barthei_HM367648	0000001100000
Zingiber_sp_MSF38	0001000000000
Zingiber_sp_MSF42	0001000000000

Zingiber_neesanum_KJ872458	0001000000000
Zingiber_nimmonii_MSF35	0001000100000
Zingiber_roseum_KJ872476	0000001000000
Zingiber_capitatum_KM983445	0000100100000
Zingiber_ligulatum_KM983446	0000100100000
Zingiber_rubens_KX088475	0000100100000
Zingiber_zerumbet_KX148588	0000000111000
Zingiber_officinale_MSF34	0001101000000
Zingiber_zerumbet_KY448306	0001100000000
Globba_sp_MF786855	0001000110000
Globba_sessiliflora_MSF21	0001000110000
Globba_bulbifera_MSF40	0001000000000
Alpinia_sp_MSF25	0001000000000
Alpinia_sp_MSF43	0001000000000
Ammomum_sp_MSF23	0001000000000
Cucurma_sp_MSF36	0001000000000
Cucurma_sp_MSF44	0001000000000
Cucuruma_sp_MSF7	0001000000000
Elettaria_cardamomum_MSF29	0001000000000
Aframomum_angustifolium	0010000000000
Aframomum_daniellii	0010000000000
Aframomum_sceptrum	0010000000000
Alpinia_aenea	0000000001000
Alpinia_arctiflora	0000000000001
Alpinia_argentea	0000000010000
Alpinia_arundelliana	0000000000001
Alpinia_bilamellata	0000001000000
Alpinia_brevilabris	0000000000010
Alpinia_caerulea	0000000000001
Alpinia_calcarata	0000001000000
Alpinia_carolinensis	0000000001000
Alpinia_coeruleoviridis	0000000001000
Alpinia_conchigera	0000001000000
Alpinia_coriacea	0000001000000
Alpinia_cylindrocephala	0000000001000
Alpinia_elegans	0000000000010
Alpinia_eremochlamys	0000000001000
Alpinia_fax	0000010000000
Alpinia_flabellata	0000000000010
Alpinia_formosana	0000001000000
Alpinia_foxworthyi	0000000000010
Alpinia_galanga2	0000000010000
Alpinia_guangdongensis	0000001000000
Alpinia_hookeriana	0000000010000
Alpinia_intermedia	0000001000000
Alpinia_japonica	0000001100000
Alpinia_latilabris	0000000010000
Alpinia_ligulata1	0000000010000

Alpinia_luteocarpa	0000000000010
Alpinia_maclurei	0000001000000
Alpinia_modesta	0000000000001
Alpinia_monopleura	0000000001000
Alpinia_mutica	0000000010000
Alpinia_nieuwenhuizii	0000000010000
Alpinia_nigra	0000000100000
Alpinia_nutans	0000000010000
Alpinia_oceanica	0000000000100
Alpinia_oxyphylla	0000001000000
Alpinia_pinetorum	0000000000010
Alpinia_polyantha	0000001000000
Alpinia_pricei	0000001000000
Alpinia_pumila	0000001000000
Alpinia_purpurata	0000000010000
Alpinia_rafflesiana	0000000010000
Alpinia_rosea	0000000000010
Alpinia_rubricaulis	0000000001000
Alpinia_rugosa	0000001000000
Alpinia_shimadae	0000001000000
Alpinia_sibuyanensis	0000000000010
ED0035529_Alpinia_sp	0000010000000
Alpinia_tonkinensis	0000000100000
Alpinia_vittata	0000000000100
Alpinia_vulcanica	0000000001000
Alpinia_warburgii	0000000001000
Alpinia_zerumbet	0000001000000
Amomum_aculeatum	0000000010000
Amomum_acuminatum	0000010000000
Amomum_aff__paratsaoko	0000001000000
Amomum_austrosinense	0000001000000
Amomum_centrocephalum1	0000000010000
Amomum_cerasinum	0000000010000
Amomum_compactum2	0000000010000
Amomum_compactum3	0000000010000
Amomum_coriandriodorum	0000001000000
Amomum_glabrum2	0000001000000
Amomum_graminifolium	0000010000000
Amomum_hastilabium1	0000000001000
Amomum_hastilabium2	0000000010000
Amomum_koenigii	0000001000000
Amomum_krervanh2	0000000010000
Amomum_krervanh3	0000000001000
Amomum_lappaceum1	0000000010000
Amomum_laxesquamosum	0000000010000
Amomum_maximum	0000001000000
Amomum_menglaense	0000001000000
Amomum_mentawaiense	0000000010000

Amomum_nemorale	0000010000000
Amomum_oligophyllum	0000000010000
Amomum_paratsaoko	0000001000000
Amomum_petaloideum	0000001100000
Amomum_pierreanum2	0000000100000
Amomum_propinquum	0000000000010
Amomum_pseudofoetens	0000000010000
Amomum_purpureorubrum	0000001000000
Amomum_putrescens	0000001000000
Amomum_quadratolaminare	0000001000000
Amomum_queenslandicum	0000000000001
Amomum_sericeum	0000001000000
Amomum_sp1	0000010000000
Amomum_sp10	0000000001000
Amomum_sp2	0000010000000
Amomum_sp3	0000010000000
Amomum_sp5	0000010000000
Amomum_sp6	0000010000000
Amomum_sp7	0000010000000
Amomum_sp9	0000000010000
Amomum_staminidivum	0000000010000
Amomum_uliginosum1	0000000010000
Amomum_uliginosum2	0000000100000
Amomum_villosum	0000001000000
Amomum_xanthophlebium	0000000010000
Amomum_yunnanense	0000001000000
Burbidgea_nitida	0000000010000
Burbidgea_schizocheila1	0000000010000
Camptandra_parvula1	0000000100000
Curcuma_albiflora	0000010000000
Curcuma_roscoeana	0000000100000
Cyphostigma_pulchellum	0000010000000
Distichochlamys_sp	0000000100000
Elettariopsis_kerbyi	0000000010000
Elettariopsis_smithiae	0000000100000
Elettariopsis_sp	0000000010000
Elettariopsis_sp5	0000000010000
Elettariopsis_stenosiphon	0000000010000
Etlingera_elatior1	0000000010000
Etlingera_triorgyalis	0000000010000
Gagnepainia_harmandii	0000001100000
Gagnepainia_thoreliana	0000000100000
Geocharis_sp1	0000000010000
Geocharis_sp2	0000000010000
Hemiorchis_burmanica	0000000100000
Hemiorchis_rhodorrhachis	0000000100000
Hornstedtia_hainanensis	0000001000000
Leptosolena_haenkei	0000000000010

Pleuranthodium_floccosum	0000000000100
Pleuranthodium_schlechteri1	0000000000100
Pleuranthodium_trichocalyx1	0000000000100
Renealmia_alpinia1	1000000000000
Renealmia_battenbergiana	0100000000000
Renealmia_cernua	1000000000000
Renealmia_thyrsoidea	1000000000000
Riedelia_sp	0000000000100
Siliquamomum_tonkinense	0000001000000
Siphonochilus_aethiopicus2	0100000000000
Siphonochilus_decorus1	0100000000000
Siphonochilus_kirkii	0010000000000
Tamijia_flagellaris	0000000010000
Vanoverberghia_sepulchrei	0000000000010
Zingiber_sulphureum	0000000010000
Zingiber_wrayii	0000000100000
Heydychium_flavescens_MHey12	0001000000000
Globba_leucantha_AY341078	0000000110000
Globba_geoffrayi_AY341087	0000000100000
Globba_albiflora_AY341091	0000000110000
Zingiber_mioga_AB047755	0000001100000
Globba_leucantha_var_bicolor_AB049255	0000000110000
Globba_cernua_AB049264	0000000110000
Globba_fecunda_AB049266	0000000010000
Globba_multifolia_AB049267	0000000010000
Globba_albobracteata_AB049269	0000000010000
Globba_atrosanguinea_AF478852	0000000010000
Globba_patens_var_costulata_AB049274	0000000110000
Globba_holttumii_AB049275	0000000010000
Globba_propinqua_AB049276	0000000010000
Globba_flavibracteata_AB049277	0000000010000
Globba_aurantiaca_AB049278	0000000010000
Globba_curtisii_AB088797	0000000010000
Zingiber_gramineum_AB088799	0000000110000
Zingiber_corallinum_AF478900	0000001010000
Zingiber_ellipticum_AF478901	0000001000000
Zingiber_gramineum_AF478902	0000000110000
Globba_xantholeuca_AY341079	0000000100000
Globba_insectifera_AY341080	0000000100000
Globba_fragilis_AY341081	0000000110000
Globba_winitii_AY341085	0000000100000
Globba_laeta_AY341086	0000000100000
Globba_pendula_AY341088	0000010110000
Globba_substrigosa_AY341092	0000000100000
Globba_variabilis_AY341098	0000000110000
Globba_adhaerans_AY341099	0000000100000
Globba_keithii_AY341105	0000000100000
Globba_flagellaris_AY341106	0000000100000

Zingiber_oligophyllum_HM116892	0000001000000
Zingiber_kawagoi_HM116893	0000001000000
Zingiber_striolatum_HM116902	0000001000000
Zingiber_smilesianum_HM116903	0000001100000
Zingiber_densissimum_HM367673	0000001100000
Zingiber_orbiculatum_HM367674	0000001100000
Zingiber_purpureum_HM367675	0000001110000
Zingiber_recurvatum_HM367676	0000001100000
Zingiber_teres_HM367677	0000001100000
Zingiber_xishuangbannaense_HM367679	0000000100000
Globba_brachyanthera_JF715488	0000000010000
Zingiber_longipedunculatum_JF715496	0000000010000
Zingiber_montanum_KC598023	0000001110000
Zingiber_parishii_KJ872474	0000000010000
Zingiber_odoriferum_KJ872468	0000000010000
Zingiber_engganoensis_KT026200	0000000010000
Zingiber_acuminatum_MN803374	0000000110000
Zingiber_loerzingii_MN803375	0000000010000